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Run on: MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Sat Jan 9 09:33:03 1999; masPar time 1049.47 Seconds 1495.136 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: >US-08-704-178-1 (1-712) from US08704178.seq (1 of 4) 712 1 ATGGACCTGCAGCTGACCCA.......GGACCACGGTCACCGTCTCCC
TACCTGGACGTCGACTGGGT.......CCTGGTGCCAGTGGCAGAGG

712

Scoring table: TABLE default Gap 6

Nmatch

STD:

Dbase 0; Query 0

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

emb155

1:em\_ba 2:em\_fun 3:em\_htg 4:em\_hum1 5:em\_hum2 6:em\_in 7:em\_om 8:em\_or 9:em\_ov 10:em\_pat 11:em\_ph 12:em\_pl 13:em\_ro 14:em\_vi 9:enbank107 15:9b\_ba1 16:9b\_ba2 17:9b\_htg 18:9b\_in 19:9b\_om 20:9b\_ov 21:9b\_ba1 23:9b\_ph 23:9b\_pl1 24:9b\_pl2 25:9b\_pr1 26:9b\_pr2 27:9b\_pr3 28:9b\_ro 29:9b\_st 30:9b\_sts 31:9b\_sy 32:9b\_un 33:9b\_vi

Mean 10.607; Variance 5.121; scale 2.071

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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### ALIGNMENTS

120	Db 60 CACAATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCC	Db 1 ATGGACCTGCAGCTGACCCAGTCTCCAGCAATCCTGCATCTCCAGGGGAGAAGGT-	Query Match 99.0%; Score 705; DB 21; Best Local Similarity 99.7%; Pred. No. 0.00e+00; Matches 710; Conservative 1; Mismatches 0	/organism="unknown" BASE COUNT 175 a 182 c 190 g 164 t ORIGIN	JOURNAL Patent: US 5587458-A 1 24-DEC-1996; FEATURES Location/Qualifiers Source 1. 711	AUTHORS King,C.Richter, Kasprzyk,P.G. and Bird,R.E. TITLE Anti-erbB-2 antibodies, combinations thereof, diagnostic uses thereof	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (15000 1 to 711)	DEFINITION Sequence 1 from patent US 5587458. ACCESSION 132406 NID 91823197
AACCTGGCTTCT     :      AACCTKGCTTCT	ATGCACTGGTA:	CTGCATCTCCAC	•-					ņ
TCASCASAASCC 120 TGGAGTCCCTGC 179		GGGGAGAAGGT- 59             GGGAGAAGGTA 60	Length 711; Indels 1; Gaps 1;			and therapeutic and		0/-0WN-133/

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92335198
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/translation="MDLOLIQSPAILSASPGEKVIMICRATPSVSYMHWYQQKPGSSP
/translation="MDLOLIQSPAILSASPGEKVIMICRATPSVSYMHWYQQKPGSSP
KPWIYTTSNLASGVPARFSGGGSGTSYSLIVSRVEAEDAATYYCOQWSRSPPTFGGGS
KLEIKGSTSGSGKSSECKGVQLOESGPEVVKPGGSMKISCKTSCYSFTGHTMNWYKQS
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             TCCGCAGCCTGACATCTGAGGACACTGCAGTCTATTATTGTGCAAG
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Shimamura, T., Hamuro, J., Nakazawa, H.,
Takeshita, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibodies which bind the interleukin-2 receptor Patent: US 558286-A 1 10-DEC-1996; Location/Qualifiers 1. .732
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                      standard;
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larity 79.8%;
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204 c 182 g
                      RNA;
                      ROD;
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Pred. No. 1.52e-280;
1; Mismatches 128;
                      732
                      В₽
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Best Local S
Matches 55
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Patent number JP 1995313188-A/1, 05
PATINOMOTO CO INC, SUGAMURA KAZUO,.

S MUS SP. (mouse)
PN JP 1995313188-A/1
PD 05-DEC-1995
PN JP 1995313188-A/1
PD 05-DEC-1994 JP 1994082836
PF 21-APR-1994 JP 1994082836
PF 21-APR-1994 JP 1994082836
PF 21-APR-1994 JP 19940817
PI SHIMAMURA TOSHIAKI, HAMURO JUN
PI KANAYAMA YUKA,
PI SUGAMURA KAZUO, TAKESHITA TOSH
PC C12P21/08,A61K39/395,A61K39/39
PC C12P21/08,C12R1:19),(C12P21/0
PC (C12P21/08,C12R1:19),(C12P21/0
PC (C12P21/08,C12R1:19),(C12P21/0
PC (Strandedness: Double;
PH Key
CC topology: Linear;
FH Key
FT source
FT source
FT source
FT source
FT mat_peptide
1. 732
FT mat_peptide
1. 732
Product="anti
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Takeshita
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08-OCT-1997 (Rel. 52, Last updated, Version cDNA encoding a monoclonal antibody against receptor gamma chain.
JP 1995313188-A/1.
                                                                                                                                                                                                                                                                                                                                                                          Sequence
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JP 1995313188-A/1
05-DEC-1995
21-APR-1994 JP 1994082836
21-APR-1993 JP 93P 94491, 0
SHIMAMURA TOSHIAKI, HAMURO JUN
                                                                                                                                                                                    CGGTGCTGGGACCAAGCTGGAGCTCAAAGTCGACAAATCCTCAGGATCTGGCTCCGAATC
                                                                                                                                      CCCAGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGCAT
TGAAGGTAAAGGTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTC
                     CAAAAGCACGCAGGTCAAACTCGAGGAGTCTGGATCTGAGCTGGTGAGGCCTGGAGCTTC
                                             CGGAGGGGGGTCCAAGCTGGAAATAAAAGGTT-CTA--CCTCTGGTTCTGGTAAATCTTC
                                                                                          GGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCATCGTTCCCCGCTCACGTT
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SUGAMURA KAZUO, TAKESHITA TOSHIICHI
C12P21/08, A61K39/395, A61K39/395, C12N1/21, C12N5/20,
C12N15/13//C12N15/06,
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Similarity 79.8%;
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BP; 180 A; 204 C; 182 G;
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Muridae; Murinae
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                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/cell_type="hybridoma"
/cell_line="GP-2"
1. 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="anti-IL-2 receptor gamma chain"
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Pred. No. 1.52e-280;
                                                                                                                                                                                                                                                                                                                           1; Mismatches 128;
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KEYWORDS
SOURCE
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                                                Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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            GAGCTGGTGAAGCCTGGAGCTTCAATGAAGATATCCTGCAAGGCTTCTGGTTACTCATTC 60
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GAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCCTGCAAGACTTCTGGTTACTCATTC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAAGCAGCCGGAACTGGGTCTACTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus r mRNA, partial U37860
                                                                                                                                                                                                                                                                                            Submitted (10-OCT-1995) Jennifer R. Swartzentruber, Institute, 3601 Spruce St., Philadelphia, PA 19104, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           Activation and negative of antibody-secreting ce
                                                                                                                                                                                                                                                                                                                                                                                                                                  Caton,A.J., Swartzentruber,J.R.,
Stark,S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g1127634
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Swartzentruber, J.R.
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1 (bases 1 )
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Vertebrata; Eutheria; Rodentia; Sciuro
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                                               h 39.7%;
Similarity 95.1%;
309; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 336)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus
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                                                                                                                                                                                                                                                                                                                                                                                   Med.
                                                                                                        /product="rearranged immunoglobulin heavy chain variable region"
/db_xref="pID:g1127635"
/translation="ELVKPGA5MKISCKASGYSFTGYTMNWVKQSHGKNLEWIGLINP YNGGTSYNGKFKGKATLTYDKSSSTAYMELLSLTSEDSAVYYCAREWLLRYFDVWGAGTTTVTVSSAKT"

81 c 85 g 78 t
                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                   /db_xref="taxon:10090"
                                                                                                                                                                                                                                                          /organism="Mus musculus"
/isolate="h922-163"
                                                                                                                                                                                                                      /cell_type="B-lymphocyte"
                                                                                                                                                                                                                                               /strain="BALB/c"
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s rearranged
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                                                         283; DB 28;
No. 7.59e-211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa;
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                                                                   Length
                                                Indels
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                                                                                                                  Query Match
Best Local S
Matches 48
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AJINOMOTO CO INC, SUGAMURA KAZUO,.
OS Mus Sp. (mouse)
PN JP 195313188-A/2
PN JP 1954138-A/2
PN JP 1954138-A/2
PN JP 19541AKI, HAMURO JUN
PN JEANAYANA YUKA,
PN JP 19541AKI, HAMURO JUN
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CDNA encoding an monoclonal antibody against receptor gamma chain.
JP 1995313188-A/2.
Mus. sp.
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E10362 standard
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08-OCT-1997 (Rel. 5
08-OCT-1997 (Rel. 5
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                                                                                                                                                                                                                                  Sequence 729
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C12P21/08,A61K39/395,A61K39/395,C12N1/21,C12N5/20,
C12N15/13//C12N15/06,
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199 A; 169 C; 182
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Shimamura, T., Hamuro, J., Nakazawa, H.,
                                                                                                                                                                       interleukin-2 receptor
Patent: US 5582826-A 3 10-DEC-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                   Unknown
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                                                                                                                                                                                                                      Takeshita, T
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AGCCTACATGGAGCTCCACAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
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                                                                                                                                 J. Exp. 1
89094248
                                                                                                                                                                   Meek,K., Hasemann,C., Pollok,B., Alkan,S.S., Brait,M., S
Urbain,J. and Capra,J.D.
Structural characterization of antiidiotypic antibodies.
that Ab2s are derived from the germline differently than
                                                                                                                                                                                                                                                                                                                                                                                                                                                        g51562
Ig kappa light chain;
house mouse.
                                                                                                                                                                                                                                                                                 Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern Medical School, 5323 Harry Hines Blud. Microbiology, Dallas Texas
                                                                                                                                                                                                                                                                                                                      Meek,K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial
Vertebrata; Eutheria; Rodo
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/cell_lin
<1. .>321
                                                     /organism="Mus musculus"
/strain="Balb/c"
                                                                                                                                                 are derived from the germline ed. 169 (2), 519-533 (1989)
                                 /db_xref="taxon:10090"
                                                                                                              Location/Qualifiers
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na 2d3 mRNA
               line="Hybridoma 2D3-K"
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for immunoglobuin kappa
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entia; Sciurognathi; N
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light chain '
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Abls
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/gene="IG kappa light chain" /note="variable region" /product="IG kappa light chain"

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AUTHORS
TITLE
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DEFINITION
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Best Local Similarity 94.8%;
Matches 290; Conservative
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                                                                     1 (bases 1 to 315)

Seemann,G. and Bosslet,K.
Antigranulocyte antibody construct, pr
Patent: EP 0585570-A 2 09-MAR-1994;
BEHRINGWERKE AG (DE)
Other publication JP 6205693 940726
Other publication CA 2101868 940206
Other publication AU 441393 940210
Other publication DE 425853 940210.
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Eukaryotae; mitochondr
Vertebrata; Mammalia;
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/db_xref="piD:q938245"
/tanslation="Q1150SPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPK
PWISATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCHQWSSNPPTFGGGTK
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/gene="IG kappa light chain"
/note="variable region"
/evidence=experimental
1...321
/organism="Mus musculus"
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                                                         Location/Qualifiers
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/note="variable region"
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                                                                                                                                                                                                                                     mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                             315 bp DNA
om Patent EP0585570.
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No. 1.91e-200;
Mismatches 14;
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                                                                                                                                                                            preparation
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RESULT 12
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Best Local s
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Local Similarity 93.3%;
hes 294; Conservative
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AGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAACCCGCTCACGTTCGGTGCTGG
                                     CTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCATCAGAGTGGAGGCTGA 239
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                                                                 ATCCTCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCG
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                            CTTCAGTGGCGGTGGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGA
                                                                                                                                                                                                                                                                                                                                                         Sequence
I51657
                                                                                                                                                                                                                                                         l (bases 1 to 315)
Seemann,G. and Bosslet,K.
Granulocyte-binding antibody constructs,
Patent: US 5645817-A 3 08-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Unknown
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                                                                                                                                                                                                                                                                                                           Unclassified.
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93.3%;
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Pred. No. 1.40e-199;
1; Mismatches 19;
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Pred. No. 1.40e-199;
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RESULT 13
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                                                                             AGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCC 243
                                                                                                                                                          GACCAAGCTGGAGAT 314
GAAATCAAA 312
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                                                                                                              AAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGC 193
                                                                                                                          AAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGC 183
                                                                                                                                                                                                                       TGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGT-CACAATGACTTGC 63
                                           ACTTATTACTGCCAGCAGTGGAGTAGTAACCCATGGACGTTCGGTGGAGGCACCAAGCTG 303
                     ACTTATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGTCCAAGCTG
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l Similarity 93.9%;
290; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linnenbach, A.J.

Molecular cloning of murine monoclonal anti-idiotypic Fab
J. Immunol. Methods 155 (1), 77-89 (1992)
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Eukaryotae;
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                                                                                                                                                                                                                                                                                                                76
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/translation="VMTQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPW
IYATSNLASGVPARESGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPWTFGGGTKLE
                                                                                                                                                                                                                                                                                                                                                                                              /gene="Ig V<kappa>"
/note="anti-idiotypic Fab;
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/gene="Ig V<down>&kgr;</down>"
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/db_xref="taxon:10095"
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manti-idiotypic
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Eutheria; Rodentia; Sciurognathi; I
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                    GTCCAAGCTGGAAATAAAA 322
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                                         GACCAAGCTGGAGATCAAA 318
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295; Conser
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Sandstrom, P., Johansson, A., Ullen, A.,
Direct Submission
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llarity 92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
/cell_line="hybridoma"
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1 GACATTCAGCTGACCCAGTCTCCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGT-CTC
                                                                                             ATCCTCCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGTTCG
                                                                                                                          CTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACCAATCAGCAGAGTGGAGGCTGA
                                                                                                                                                                                                                                                                                                                            AATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATACACTGGTACCAGCAGAAGCCAGG
AGATGCTGCCACTTATTACTGCCAGCAGTGGAGTGGTAACCCGCTCACGTTCGGTGCTGG
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 318)
1 (bases 1 to 318)
Sandstrom,P., Johansson,A., Ullen,A., Behravan,G. and Stigbrand,T.
Differences in sequence and affinity between three monoclonal anti-idiotypic antibodies against one anti-placental alkaline phosphatase idiotypic antibody
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="monoclonal antibody aH7:38 IgG1 light chain"
/db_xref="PID:g3044132"
/translation="DIO:g514153"
PWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSGNPLTFGAGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="anti-idiotypic antibody against anti-placental
lkaline phosphatase antibody; variable region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 268; DB 28;
Pred. No. 7.55e-198;
1; Mismatches 22;
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IgG1 light chain mRNA,
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ATAAAAGGT 325
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Parslow,T.G., Blair,D.L., Murphy,W.J. and Granner,D.K.
Structure of the 5' ends of immunoglobulin genes: A novel conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g196460
C-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa.
Mouse 702/3 cell DNA.
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/db_xref="taxon:10090"
<776. .824
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/number=2
1338. .>1369
/note="kappa cds intron J-C"
273 c 253 g 440 t
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/trans1ation="mdpqvqlfspfllisasvimsrgqivlsqspailsaspgekvimt
Crassssysymmyqokpgsspkpwiyatsnlasgvparfsgsgsgtsysltisrveae
Daatyycoomssnprffgggtkleik"
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                                                                                                                                                                                                                                                 n.a. - n.a. database search, using Smith-Waterman algorithm
                                                >US-08-704-178-1 (1-712) from US08704178.seq (1 of 712
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1 ATGGACCTGCAGCTGACCCA......GGACCACGGTCACCGTCTCC 712
TACCTGGACGTCGACTGGGT......CCTGGTGCCAGTGGCAGAGG
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834.616 Million cell updates/sec
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Description:
Perfect Score:
N.A. Sequence:
Comp: Searched: Nmatch Scoring table: STD : TABLE default Gap 6 188442 segs, 68026449 bases Dbase 0; Query 0 ×

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
1:part1 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part20 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 8.732; Variance 5.071; scale 1.722

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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264	265	266	266	266	279	363	375	375	410	699	701	705	Score	
37.1	37.2	37.4	37.4	37.4	39.2	51.0	52.7	52.7	57.6	98.2	98.5	99.0	Match	Ouerv
9208	384			462 :									Length DB	
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Q65629	Q65630	T34542	T99435	T31541	Q73679	Q73678	Q55181	T65007	T91615	T17728	Q55180	T65006	ID	
Vector contg. TCAE 8	Murine variable regio	Monoclonal anti-idiot	Anti-idiotype antibod	3H1 heavy chain varia	Fv(GP-4) immunosuppre	Fv(GP-2) immunosuppre	Sequence encoding the	Single-chain anti-erb	cDNA encoding an anti	Anti-erbB2 scFv cDNA.	Sequence encoding the	Single-chain anti-erb	Description	
3.17e-166	5.98e-167	1.13e-167	1.13e-167	1.13e-167					1.02e-272	0.00e+00	0.00e+00	0.00e+00	Pred. No.	

45	44	43	42	41	40	39	38	37	36	35	34	ယ္သ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
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encoding l	imeric antibody li	neavy chain.	main of antibod	lonal antibody	noclonal antibody	2 chimeric antib	i-IL2R-alpha anti	e A5B5	nce encoding a	e encoding d	CC49/212 SCA	2 SC.	des Variable reg	asmid PAH	lasmid pAH	smid pAH	id pAH4625.	ric 128.1 VH,	s A5B7 antibo	2 light chain v	o N	2H7 antibody	e 2H7 antibody	antibody light	ing sequence for	ght chain van	3	Ϋ́	-Factor IX MAD	use anti-human Fac	Anti-Factor IX MAb ch
.44e-1	.22e-1	.30e-1	.23e-1	.23e-1	.23e-1	2.94e-15	.94e-1	.05e-1	.05e-1	.98e-1	.98e-16	.98e-1	.74e-16	.05e-1	.05e-	.05e-16	.05e-16	.05e-1	.05e-1	.93e-1	.68e-1	.68e-1	.68e-1	.68e-1	.68e-1	.68e-1	.68e-1	.68e-1	.68e-1	.68e-1	.68e-1

### ALIGNMENTS

SULT	ia 1
	T65006 standard; cDNA; 711 BP.
	(first entry)
	Single-chain anti-erbB2 antibody e23(Fv) cDNA.
	antibody; variable region;
	cancer; ovarian cancer; non-small cell
	Mus musculus.
	Synthetic.
	Key Location/Qualifiers
	mat_peptide 1711
	/*tag= a
	/product= e23(Fv)
	US5587458-A.
	24-DEC-1996.
	07-OCT-1991; 772270.
	07-OCT-1991; US-772270.
	Bird RE, Kasprzyk PG, King CR;
	064831/06.
	P-PSDB; W15185.
	chain antibodies specific for erbB-2 protein, gp
	ο.
	cells expressing this protein
	The present cDNA sequence codes for a claimed single-chain antibody,
	designated e23(Fv), which binds to erbB-2. Monoclonal antibody e23
	generated by immunising mice
	10
	by standard techniques. Messenger RNA coding for the anti-erbB-2
	monoclonal antibody was isolated and converted to cDNA. Regions
	coding for the heavy- and light- chain variable regions were then
	amplified by PCR and joined via a sequence encoding a peptide
	linker. The resulting single-chain antibody is useful for in vitro

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Q55180;
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Single chain
WO9400136-A.
06-JAN-1994.
21-OCT-1992;
30-JUN-1992;
                                                       monoclonal Synthetic.
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                                                                       ce encoding the single chain chain anti-erbBl antibody;
                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 711; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of tumour cells which overexpress the erbB-2 gp185 of breast, ovarian and non-small cell lung carcinomas, coupled to a cytotoxic agent, to treat such tumours. 711 BP; 175 A; 182 C; 189 G; 164 T;
                                                                antibody;
U08545.
US-906555.
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/*tag= a
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                                                                       therapy;
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Matches 70
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Example; Fig
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Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kasprzyk PG, King
WPI; 94-025878/03.
P-PSDB; R45442.
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CATGGAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGAGGGT
                                                    catggagctcctcagtctgacatctgaggactctgcactctattactgtgcaaggagggt
                                                                                   CAACCAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTA
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llarity 99.6%;
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of human
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nich recognise different
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Pred. No. 0.00e+00;
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RESULT 3 ID T17728

standard;

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Matches
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14-MAR-1996.
14-SAUG-1995; U10740.
06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibition of proliferation or survival of, esp. malignant erbB2, cells - by introducing nucleic acid mol. encoding antibody homologue which is expressed and binds, pref. erbB2, protein intracellularly claim 42: Page 29-30; 48pp; English.

A nucleic acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a single chain Fv fragment (R94020) that binds a human erbB2 oncoprotein. The anti-erbB2 sFv portion is obtained by PCR using e33sCFv plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibody homologue within e.g. an epithelial carcinoma cell. Intracellular expression of the homologue inhibits surface expression of erbB2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Curiel DT, Deshane J; WPI; 96-171307/17.
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Curiel DT, Deshane J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intracellular antibody homologue; single gene therapy; ds.
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21-MAY-1996 (first entry)
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AGGTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGAT
                                                                                                                                                                      aggtgtgcagctgcaggagtcaaggacctgaggtggtcaagcctggaggtttcaatgaagat
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707; Conser
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omologue; single chain antibody; scFv;
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Pred. No. 0.00e+1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing Single chain Fv antibody in Escherichia coli - by expression in an inclusion body, followed by protein folding or by co-expression with a chaperonin as a soluble fraction claim 4; Page 6-7; 9pp; Japanese.

Claim 4; P
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Best Local S
Matches 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 4
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WPI; 97-474306/44.
P-PSDB; W25784.
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Pred. No. 1.02e-272;
1; Mismatches 104;
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                                                                                                                                                                                             Fig. 1. Single chain antibodies specific for erbB-2 protein, gp185 - with plabels or cytotoxin, useful for detection and treatment of tumour cells expressing this protein

Example 9; Columns 27-30; 28pp; English.

The present cDNA sequence codes for a claimed single-chain antibody, which binds to erbB-2. Monoclonal antibody e21

Catesignated e21(Fv), which binds to erbB-2. Monoclonal antibody e21

Catesignated by immunising mice with NyerbB-2 cells overexpressing the gp185 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-crbB-2 coding for the heavy- and light-chain coding for the new of a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gp185 cmarker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours.

So Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
                                                                                                                               Query
Best I
                                                                                                          Matches
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24-DEC-1996:
07-OCT-1991: 772270.
07-CCT-1991: US-772270.
30-JUN-1992: US-906555.
14-MAY-1993: US-661092.
(ARON-) ARONEX PHARM INC.
Bird RE, Kasprzyk PG, Ki
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T65007;
05-JUN-1997
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Single-chain anti-erbB2 antibody e21(Fv) cDNA.
Single-chain antibody; variable region; light chain; heavy
breast cancer; ovarian cancer; non-small cell lung carcinon
immunodiagnosis; treatment; cytotoxic agent; erbB-2; ds.
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TGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATG
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Similarity 79.3%;
511; Conservative
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(MOLE-) MOLECULAR ONCOLOGY I
Kasprzyk PG, King CR;
WPI; 94-025878/77
gp185
Example; Fig 8; 37pp; English.
The source of human erbB-2 protein for the prodn. of antibodies 2 and 21 (055180/R45442; 055181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (NerbB-2). Abs no. 21 and 23 are directed against the extracellulated domain of gp185 erbB-2. Nude mice manipulated to produce rapidally growing tumours were used in a trial of the efficacy of the Abs animals given a combination of the 2 Abs, tumours completely regreesed after 11 days.

Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-1994.
21-OCT-1992;
30-JUN-1992;
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Q55181;
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073678;
09-MAY-1995 (first entry)
E Fv(GP-2) immunosuppressive.
W MAb; monoclonal antibody; hybridoma; in
W MAb; monoclonal antibody; fybridoma; in
W Fv; antibody variable region; GP-2; Fv(
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Matches
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EP-621338-A.
26-OCT-1994.
21-APR-1994; 106257.
21-APR-1993; JP-094491.
07-MAR-1994; JP-036065.
                                                                                         Hamura J,
Takeshita
 Immunosuppressant polypeptide interleukin-2 response Claim 17: Page 29; 37pp; Engl: MAb capable of binding to the
                                                            P-PSDB; R60780
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                                                                                                        Kanayama
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larity 79.3%;
Conservative
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                                                                                                          Nakazawa
                  English
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Pred. No. 4.34e-247
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                                                                                                                                                                                                                                           Fv(GP-2);
   chain
                                             ability
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                                                                                                          Shimamura
    of,
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    the
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 Mus sp.

EP-621338-A.

26-OCT-1994.

21-APR-1994;

21-APR-1993;

07-MAR-1994;
                                                                                       immunosuppressive;
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Query Match
Best Local S
Matches 55
Q73679 standard; DNA; 729 BP.
Q73679;
Q73679:
Q9-MAY-1995 (first entry)
FV(GP-4) immunosuppressive.
MAD; monoclonal antibody; hybri
FV; antibody variable region; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thus of blocking the II-2 response, is produced by mouse line GP-2 (FERM BP-4641). DNA encoding the variable regiths MAb was expressed in E. coli, yielding Fv(GP-2) with immumosuppressive activity.

Sequence 732 BP; 180 A; 204 C; 182 G; 166 T
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                                                                                                                                                                                                                                                                           GAAGCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTTATTAATCCTTACAATGGTGA
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l Similarity 79.8%;
550; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 363; Pred. No. 2.1
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d. No. 2.58e-238;
Mismatches 128;
                                                                                                                      680
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106257. JP-094491. JP-036065.

hybridoma; interleukin-2;

GP-4;

Fv(GP-4);

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RESULT
ID T
AC T
DT 11
DE 31
KW A1
KW C2
KW V2
OS M
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Best Loc
Matches
        3H1 heavy chain variable region cDNA.
Anti-idiotype; monoclonal antibody; MAb; 3H1; CEA; carcinoembryonic antigen; cancer; gene therapy; im vaccine; genetic immunisation; heavy chain; VH; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunosuppressant polypeptide - has ability to block interleukin-2 response Claim 18; Page 29; 37pp; English.

MAB capable of binding to the gamma chain of the IL-2 receptor, and thus of blocking the IL-2 response, is produced by mouse hybridoma thus of blocking the IL-2 response, is produced by mouse hybridoma Line GP-4 (FERM BP-4640). DNA encoding the variable region of this MAB was expressed in E. coli, yielding Fv(GP-4) with
                                                             T31541;
18-SEP-1996
                                                                                         T31541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Sequence 729 BP; 199 A;
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                                                                                                                                                       agcctacatggagctccacagcctgacatctgaggactctgcagtctattactgtgcaag
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                                                                                                                                                                                                                                                              AGGTAAAGGTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAAT
                                                                                                                                                                                                                                                                                                                                                                    aagcacgcaggtcaaactcgaggagtctggacctgagctggtgaagcctggggcttcagt 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caccatcacatgtcgagcaagtgggaatattcaccaattattagcatggtatcagcagaa 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTA
                                                                                                                                                                                             TAACTACAACCAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCAC
                                                                                                                                                                                                                                               GCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTTATTAATCCTTACAATGGTGATAC
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                                                                                                                                          AGCCTACATGGAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
487; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kanayama
                                                               (first entry)
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                                                                                       cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.2%;
73.8%;
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Pred.
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No. 4.18e-17
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                       immunotherapy;
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CC (Ac DNA clone (T31541) codes for the heavy chain variable region (CYM) (R98411) of 3H1, a murine monoclonal anti-idiotype antibody that mimics a specific epitope of the 180,000 mol.wt.

CC carcinoembryonic antigen (CEA) and which elicits an immune response in patients with advanced CEA-associated disease, e.g. colorectal concer. It was obtd. by PCR amplification of 3H1 hybridoma DNA (see also T31545-46). The isolated polynucleotide, and/or a polynucleotide (see also T31540) coding for the VL region (R98410) cof 3H1 can be used to design probes and primers, in expression systems, and in pharmaceutical applns, including vaccines, gene therapy and genetic immunisation, partic. against cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches 31
                                                                    Anti-idiotype antibody 3H1 heavy chain variable region Anti-idiotype antibody 3H1; carcinoembryonic antigen; C tumour-specific antigen; tumour; colorectal cancer; lun adenocarcinoma; therapy; ss.

Mus musculus.
                                                                                                                                 T99435 stand
T99435;
T99435;
27-APR-1998
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28-DEC-1995;
28-DEC-1994;
 WO9738725-A1.
23-OCT-1997.
11-APR-1997; U05953
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l Similarity 90.08;
316; Conservative
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US-365484.
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Pred. No. 1.13e-167;
0; Mismatches 32;
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Best Local
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               04-JUL-1996.
28-DEC-1995; U17105.
28-DEC-1994; US-365484.
(KENT) UNIV KENTUCKY.
Chatterjee M, Chatterjee S
WPI; 96-321809/32.
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12-APR-1996; US-631085.
(KENT) UNIV KENTUCKY.
Chatterjee M, Chatterjee S
WPI; 97-526218/48.
                                                                                                                                                                                                                                                                                                          11-OCT-1996 (first entry)
Monoclonal anti-idiotype antibody 3H1 VH cDNA.
Anti-idiotype antibody; monoclonal antibody; CEA;
carcinoembryonic antigen; tumour-associated antigen;
                                                                                                                                                                    WO9620219-A2.
                                                                                                                                                                                                                                        Mus
                                                                                                                                                                                                                                                                                           vaccine;
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T34542;
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Q1-FEB-1995
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03-NOV-1993;
(IDEC-) IDEC
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A cDNA clone (T34542) codes for the heavy chain variable region (R99687) of monoclonal anti-idiotype antibody 3H1 (ATCC HB 1200 It was obtd. by PCR amplification (see also T34543-44) of cDNA derived from 3H1 hybridoma cells. Anti-idiotype antibody 3H1 elicits a specific immune response to a unique epitope of carcinoembryonic antigen (CEA) that is not present on other members of the CEA family or on normal adult tissues. 3H1 can be used as a vaccine to elicit immune responses in patients
                                                                                                                           Treating B cell lymphoma with chimeric antibody causing rapid depletion of peripheral B cells, a antibodies and hybridomas Disclosure; Fig 4; 101pp; English.

The sequence is the murine variable region light
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Murine variable region light chain from 2BS.
B cell lymphoma chimeric antibody; CD20; per
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Sequence 462 BP; 106 A; 124 C; 117 G; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
W09411026-A.
                                                                Sequence
                                                                                    See also
                                                                                                           murine anti-CD20 monoclonal antibody
                                                                                                                                                                                                                                            P-PSBD; R55214.
                                                                                                                                                                                                                                                                 WPI; 94-183162/22.
                                                                                                                                                                                                                                                                                     Refime
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12-NOV-1993;
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                                                                  Q65629-35.
384 BP;
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US-149099.
C PHARM CORP.
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37.2%;
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Pred. No. 1.13e-167;
0; Mismatches 32;
Score 265;
Pred. No. !
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y 2BS.
                                                                                                                                                                                                                                                                                                            Newman
; DB 11;
5.98e-167;
                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peripheral blood cells;
                                                                                                                              light
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also new
                  Length 384
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Best Local S
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26-MAY-1994; U10953.
12-NOV-1993; US-978891.
3-NOV-1993; US-149099.
(IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                     Treating B cell lymphoma with chimeric antibody - against CD20, causing rapid depletion of peripheral B cells, also new antibodies and hybridomas plisclosure; Fig 3; 101pp; English.

The sequence shows a vector contg. TCAEB, a gene encoding a chimeric anti-CD20 antibody for treatment of B cell lymphomas. TCAEB contains 4 transcriptional cassettes, human Ig light and heavy chain constant regions, dihydrofolate reductase, neomycin phosphotransferase and murine variable regions. The vector can be used to produce antibodies which cause depletion of peripheral blood B cells, including those associated with lymphoma. They mediate complement-dependent lysis and lyse target cells by antibody-dependent cellular
                                                                                                                                                                                                                                                                                                                                                                                       Reffme; WPI; 94
    1176
                                                      1116
                                                                                                          1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B cell lymphoma cell lysis; ss.
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Q65629;
Q1-FEB-1995 (first entry)
                                                                                                                                                                                      See also Q65629-35.
Sequence 9208 BP;
                                                                                                                                                                                                                cytotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson DR,
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ccctggatttatgccacatccaacctggcttctggagtccctgttcgcttcagtggcagt 1235
                        GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAA 136
                                          gccagctgaagtgtaagttacatccactggttccagcagaagccaggatcctcccccaaa 1175
                                                                                             cccagtctccagcaatcctgtctgcatctccaggggagaaggt-cacaatgacttgcagg 1115
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ma chimeric antibody; CD20; peripheral blood
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                                                                                                                                              37.1%;
93.2%;
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Pred. No. 3
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3.17e-166;
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Best Local S
Matches 28
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24-JUL-1997.

17-JAN-1997; U00759.

24-CCT-1996; US-029119.

21-JAN-1996; US-010108.

3 17-JAN-1996; US-010108.

4 (SMIK) SMITHKLINE BEECHAM CORP.

4 (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

5 Blackburn MN, Church WR, Feuerstein GZ, Gross MS;

1 Nichols AJ, Padlan EA, Patel AH, Sylvester DR;

1 WPI; 97-385117/35.
                                                                                                                                                                                                                                                                                                             Example 7; Page 128; 150pp; English.

This CDNA sequence encodes a mouse-human chimeric antibody
light chain (W24532) in which the variable region is derived
from mouse anti-human factor IX monoclonal antibody BC2 cDNA (See
T79899) and human sequences from the immunoglobulin RF-TS3'CL
framework. It was obtained by PCR amplification (See T79897-98)
of BC2 cDNA and insertion of the PCR product into F9HZHC 1-3 cDN4
(See T77374). Claimed anti-Factor IX chimeric antibodies are
useful in the treatment of thrombosis.

Sequence 318 BP; 79 A; 91 C; 78 G; 70 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-Factor IX MAb chimeric light chain cDNA.
Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody; chimeric antibody; antibody engineering; light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T79900
T79900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric Homo sapiens.
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric antibody; ant
Chimeric Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; W24532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-DEC-1997
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tattactgccagtggagtattaacccacggacgttcggtggaggcaccaagctggaa
                                                                                                                                                                                                                      tattactgccagcagtggactagtaacccacccacgttcggaggggggaccaagctggaa
                                                    gggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccact
                                                                                             CCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGT
                                                                                                           GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAA
                                                                                                                                                                gccagctcaagtgtaaattacatgcactggtaccagcagaagccaggatcctcccccaaa 132
                                                                                                                                                                                                      CCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGCAGG
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                                                                                                                                                                                                                                                               286;
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                       36.98;
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                                                                                                                                                                                                                                                            Score
Pred.
1; M
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                                                                                                                                                                                                                                                                         263;
No. 1.
                                                                                                                                                                                                                                                            DB 34; I
..68e-165;
ches 18;
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This CDNA sequence encodes the light chain variable region (see W24520) of mouse anti-human Factor IX monoclonal antibody RC2. Claimed humanised antibodies (see W24510-18) contain CDRs (see CW2504-09) of BC2 heavy and light chains inserted into framework regions of selected human antibody sequences. They have self-limiting neutralising activity, and are useful as anticoagulant agents in treatment of thrombosis associated with myocardial infarction, unstable angina, atrial fibrillation, stroke, renal damage, pulmonary embolism, deep vein thrombosis, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulation, sepsis, or artificial organs, shunts or prostheses (claimed). Also claimed are chimeric antibodies (see T79900), and Fab and F(ab')2 fragments. The claimed antibodies do not cause uncontrolled bleeding (contrast heparin and warfarin) since they sequence 321 BP; 78 A; 92 C; 79 G; 72 T;
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 28
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Mouse anti-human Factor IX antibody BC2 light chain cDNA.
Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody; humanised antibody; antibody engineering; light chain; CDR; complementarity determining region; myocardial infarction; angina; atrial fibrillation; stroke; kidney damage; pulmonary embolism; deep vein thrombosis; coronary angioplasty; pulmonary embolism; deep vein thrombosis; coronary angioplasty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 15
T77377 standard; cDNA; 321
T77377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibition Example 5; Page 64; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYVE-, Church
Blackburn MN, Church
Blackburn MN, Church
Padlan EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9726010-A1.
24-JUL-1997.
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WPI; 97-385117/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
(UYVE-) UNIV VERMONT & Feuerstein GZ, Gross
Blackburn MN, Church WR, Feuerstein GZ, Gross
Nichols AJ, Padlan EA, Patel AH, Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-1997; U00759.
24-CCT-1996; US-029119.
17-JAN-1996; US-010108.
(SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
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                                                                                                                gccagctcaagtgtaaattacatgcactggtaccagcagaagccaggatcctcccccaaa 132
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tattactgccagcagtggagtattaacccacggacgttcggtggaggcaccaagctggaa
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93.5%;
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Pred. No. 1.68e-165;
1; Mismatches 18;
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δõ Search completed: Sat Job time: 122 secs. Jan 9 12:38:18 1999

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat Jan 9 11:32:13 1999; MasPar time 954.49 Seconds 1335.831 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: >US-08-704-178-1 (1-712) from US08704178.seq (1 of 712 4

1 ATGGACCTGCAGCTGACCCA.......GGACCACGGTCACCGTCTCCC
TACCTGGACGTCGACTGGGT..........CCTGGTGCCAGTGGCAGAGG 712

Scoring table: TABLE default Gap 6

Nmatch

STD :

Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: embl-est55

1:em\_est1 2:em\_gss1 3:em\_gss2 4:em\_gss3
genbank-est107
5:gb\_est1 6:gb\_est10 7:gb\_est11 8:gb\_est12 9:gb\_est13
10:gb\_est14 11:gb\_est15 12:gb\_est16 13:gb\_est17
14:gb\_est18 15:gb\_est19 16:gb\_est2 17:gb\_est20
18:gb\_est21 19:gb\_est3 20:gb\_est4 21:gb\_est5 22:gb\_est6
23:gb\_est7 24:gb\_est8 25:gb\_est4 21:gb\_gss1 27:gb\_gss2
28:gb\_gss3 29:gb\_gss4

Statistics:

Mean 10.709;

Variance 1.855; scale 5.772

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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80 80	8888	1146 110 92	232	Score
11.4 11.4 11.2	11.5	20.5 20.5 15.4 12.9	32.6	Query Match
209 488 333	279 379 393	345 345	396	Query Match Length DB
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T28938 H25625 AA300732	AA300571 AA291381 T27593	A1180569 A1007196 AA569186 AA710291 AA318377	AA691311 AA592800	Ħ
EST61186 Homo sapiens y148905.rl Homo sapien EST13847 Testis tumor	EST13661 Testis tumor zt44902.rl Soares ovar EST100653 Homo sapiens	uC/UIU9.rl Soares mous ua73g04.rl Soares 2NbM nm30d10.sl NCI_CGAP_Li vt53a04.rl Barstead mo		Description
4.51e-118 4.51e-118 6.81e-116		3.63e-298 1.74e-265 1.05e-182 2.72e-142	0.00e+00 0.00e+00	Pred. No.

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## ALIGNMENTS

	source	FEATURES								COMMENT	JOURNAL	TITLE					AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION		DEFINITION	LOCUS	RESULT 1
<pre>/organism="Mus musculus" /strain="FVB/N" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified</pre>	1396	seq primer: "28m13 rev2 ET from Amersham. Location/Qualifiers	IMAGE Consortium (info@image.llnl.gov) for further information.	<pre>This clone is available rovalty-free through LLNL : contact the</pre>	Fax: 314 286 1810	Tel: 314 286 1800	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	Washingto University School of Medicines	Contact: Marra M/Mouse EST Project		Unpublished (1996)	The WashU-HHMI Mouse EST Project	Waterston, R.	Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and	Schellenberg K. Steptoe M. Tan F. Hiderwood K. Moore B.	Coicola Kinaba T Ianv M Ia M Martin I Morric M	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,	1 (bases 1 to 396)	Eukaryotae; metazoa; Chordata; vertebrata; mammaila; Eutherla; Dodontia: Columnormath; Muridao: Murimao: Mi		house mouse.	EST.	g2692247	AA691311	immunoglobulin kappa light chain (MOUSE);, mRNA sequence.	vs14101.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA	AA691311 396 bp mRNA EST 16-DEC-1997	

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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA592800 344 bp mRNA EST 17-SEP-1997 vo25g11.rl Barstead mouse irradiated colon MPLRB7 Mus musculus clone 1050980 5' similar to gb:x67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence. AA592800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g2406463
EST.
Fax: 314 400 1012
Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL;
                                                                                                                                                                                                                                                                              Rodentia; Sciurognath; Muridae; Murinae; Mus.

1 (bases 1 to 344)
Marra, Hilter, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                           Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                       The WashU-HHMI Mouse Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                   Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;
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/dev_stage="8 weeks"
/lab_host="DH10B"
/ 107 c 91 g 94 t
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Pred. No. 0.00e+00;
1; Mismatches 29
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                                                                                                                                                                                                                                                                                                                                                                                                         CCACTTATTACTGCCAGCAGTGGAGTCGTA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGTAGCTCTGGGACCTCCTACTCTCTCACAATCAGCAGAATTGAGGCTGAACATGCTG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAAACATGGATTTATGATACATCTAAACTGGCTTCTGGAATCCCTGCTGCTTCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAG-GGGAGAAGGTACACAATGACTT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCC
                                                                                                                                                                                                                                               mRNA, com
AI180569
                                                                                                                                                                                                                                                                          AI180569 310 bp mRNA EST 08-OCT-1998 uc70f09.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone 1431017 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene
                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata;
Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226;
                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                g3731207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality Seq primer: -28ml3 rev2 ET from Amers! High quality sequence stop: 1.

Location/Qualifiers
Unpublished (1996)
                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
                                                                                                                                                                                                                                                               complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 3']; double-stranded CDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead." /db_xref="ftaxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Barstead mouse irradiated colon /dev_stage="8 weeks" /lab_host="DH10B" <1. >344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus |
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .>344
91 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 179; DB 9;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 344;
                                                                                                                                      Mus.
                                                                                                                                                        Mammalia; Eutheria;
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RESULT
LOCUS
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                                             SOURCE
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                                                                KEYWORDS
                                                                                                                                                                                          DEFINITION
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Best Local :
                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                               CAAAAGTTCAAGGGCAAGGCAGCATTGACTGTAGACACATCCTCCAGCACAGCCTACATG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGACAGGGCATTGAGTGGATCGGAGAGATTGATCCTTCTGATAGCTATACCTAACTACAAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGTAAAACAGAGGCCCT 121
                                                                                                                                                                                                                                                                                        GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
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                                                                g3216753
EST.
                                                                                                         (MOUSE);,
AI007196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                       AI007196 294 bp mRNA EST 12-JUN-1998 ua73g04.rl Soares 2NbMT Mus musculus cDNA clone 1363158 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE Consortium (info@image.llnl.gov) for MGI:915085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
                   Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: -28m13 rev2 ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="mammary g
/dev_stage="4 weeks"
/lab_host="DH10B"
a 77 c 85 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares mouse mammary gland NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="1431017"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.5%;
79.3%;
                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 160; DB 18;
Pred. No. 3.63e-298;
0; Mismatches 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Louis, MO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jh LLNL ; contact the
further information.
                                                                                                                                                                                                                                                                                                                                 291
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                                                                                                                                                                                                                                                                                                               365 GTGCAGCTGCAGGAGTCAGGACCTGAGG-TGGTGAAGCCTGGAGGTTCAATGAAGATATC 423
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                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                 TGCAGCTCAGCAGACTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAG
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                                                                                                                                                                                                                                                                                                                                                GTCCAACTGCAGCAGCCTGGGGCTGAGCATGGTGAGGACTGGGTCTTCAGTGAAGCTGTA 61
                                                                                                              CCAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACA-
                                                                                                                                             TCAAAAGTTCAAGGACAAGGCCACATTGACTGTAGACAAATTCACCAGCACAGCCTACAG
                                                                                                                                                                               TATACAAGGCATTGAATGGATTGGTAACATTGACCCTTCAGATAGTGGAACTCACTACAA
σı
                                              TGGAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
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1 (bases 1 to 294)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu.
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor quality Seq primer: -28ml3 rev2 ET from Amers High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:896378
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                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Thymus"
/dév_stage="4 weeks"
/lab_host="DH10B"
a 68 c 77 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soares and M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="1363158"
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                                                                                                                                                                                                                                                                                                                                                                                              20.5%;
                                                                                                                                                                                                                                                                                                                                                                               Score 146; DB 15;
Pred. No. 1.74e-265;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 294;
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                    338 GAGCTTAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCGAG 387
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                                                                                                                                                                                                                                                                                                                                           GTCCAACTGGTGCAGTCTGGGGCTGAGGTGAAGATGCTTTCC 157
GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                                                                                                    CAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTATATG 337
                                                                                                                                                                                                                                                                             TGTAAGGCATCTGGATTCACCCTCACCAACTGCCATATGCACTGGGTGCGACAGGCCCCT 217
                                                                                                                                                                                                                                                                                                                      GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCC 424
                                                                                                                                                         GGGCAAGGGCTTGAGTGGGTGGGAATGATCAATTCTAGTGATGGTTATATAAGTAACGCA 277
                                                                                                                                                                                                                                        TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
                                                                                                                                                                                                                                                                                                                                                                                                       200; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA569186 387 bp mRNA EST nm30d10.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone I similar to gb:L02325 IG HEAVY CHAIN PRECURSOR V-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing C Clone distribution: NCI-CCAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 387)
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AA569186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 1722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer: -40ml3 fwd. ET from Amersham
h quality sequence stop: 284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:1061683"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
<1...>387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Organism="Homo sapiens"
/note="Yector: pAMP10; mRNA made from liposarcoma, cDNA
/note="Yector: pAMP10; mRNA made from liposarcoma, cDNA
made by oligo-dT priming. Non- directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%;
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95 c
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 110; DB 9; L
Pred. No. 1.05e-182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jeffrey Medeiros, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE:1061683
I REGION (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Project (CGAP),
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                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                   Query Match 12.9%;
Best Local Similarity 66.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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  132
                                                                                                                                                                                   14
                       CTAGAGCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATCGCTTCACAG
                                                                                                                                                                                   TGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGC
CCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTG
                                                                                                                  AAGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAAGAGAAACCAGGGCAATCTC
                                                                                                                                                                                                                              TGACCCAGTCTCAAAAATTCATGTCCACATCAGCTGGAGACAGGGT-CAGCGTCACCTGC
                                                                                        AGGGCCACCCCAA-GTGTA-AGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 345)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vt53a04.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA cLone 1166766 5' similar to gb:X002484_rnal IG KAPPA CHAIN PRECURSOR V-IV REGION (HUMAN); gb:J00560 mouse ig kappa mrna from mopc21 6 other myeloma mrna 3' (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g2720209
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:632678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: -28m13 rev2 ET from Amersham
n quality sequence stop: 140.
                                                                                                                                                                                                                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGCATCCTTG], digested with NOt I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/Strain="FVB/N"
/Strain="FVB/N"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained
from 8 week old mouse. Colon was harvested 72 hours after
irradiation with 1400 Gys. 1st strand CDNA was primed
with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="8 weeks"
/lab_host="DH10B"
81 c 88 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="1166766"
/clone_lib="Barstead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Locat:
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                                                                                                                                                                                                                                                                         Score 92; DB 11; LC
Pred. No. 2.72e-142;
Mismatches 99;
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J. Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G. L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Triftial accessment of human gene divergity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAGTATTTCTGTCAGCAATATAACAGCTTTCCGTACACGTTCGGAGGGGGGACCAAGC
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AA318377
g1970863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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EST20620 Spleen I Homo
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arkerlav@tigr.org
                                                                              <u>^</u>
                                                                                                                                                                                     note="Organ: spleen; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
//db_xref="ATCC (inhost):119058"
//db_xref="taxon:9606"
//clone_lib="Spleen I"
                                                                                                           /dev_stage="adult, 23 yrs"
                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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Best Local Similarity 67.1%;
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 TGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGTCCAAGCTGGAAATAAAAGGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Frasser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTTCCAGTAGCCCTTGGACGTTCGGCCAAGGGGNCCAAGGTGGCAATCAAACGNACT 272
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                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: THC166571
Contact: Kerlavage, AR
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                             For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                     Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                          Fax: 3018699423
                                                                                                                                                                                                                                                                                                          Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
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                                                                                                                 primer: M13 Reverse
/note="Organ: testis;
                               /organism="Homo sapiens"
                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (6547 Suppl),
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Pred. No. 4.99e-129;
1; Mismatches 77;
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similar to similar
(GB:M18512), mRNA
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Vector: pBluescript SK-; Site\_1:

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mRNA
BASE COUNT
ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGAAGTT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGAAGTT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACAAGGGCTTNAGTGGATGGGATGGATCAACCCTAAAAGTGGTGGCACAAACTATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1576 Std Error: 0.00
                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                  Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lenon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA291381 379 bp mRNA EST 5. 5. sinilar to gb: M18512 IG HEAVY CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMAN);, mRNA sequence AA291381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                               primer:
                                                                                                                                          rt Length: 1576 Std Error: 0.00 primer: -28m13 rev2 ET from Amersham quality sequence stop: 361.
Location/Qualifiers
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larity 72.3%;
Conservative
                                                                                                                                                                                                                                           est@watson.wustl.edu
/db_xref="taxon:9606"
/clone_lib="Testis tumor"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECORI; Site_2: XhOI"
/db_xref="ATCC (inhost):192212"
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<1. .>279
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0; M
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Best Local
                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of CDNA Sequence
Contact: Venter, JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAGTTTTCAGGACAGAGTCAGCTTGACCACTGACATCCACGAATACAGCCTACATG
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191; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T27593 393 bp mRNA EST 06-SEP-1995 EST100653 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human primer=M13 Reverse library=Human Pancreas Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           light chain, T27593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 393)
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/db_xref="taxon:9606"
/clone="725234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Pharmacia). Library constructed by Bento Soares and
M Fatima Bonaldo "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares ovary tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B (ampicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="ovarian"
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Pred. No. 2.95e-
0; Mismatches
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No. 2.95e-120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae;
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BASE

FEATURES

ORIGIN

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACAC 63
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gooayne, J.D.,
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Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGTTCAGTGGCTCTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGACTTGCAGGGCCCACCCCAAGTGTAAGTTACATGC---ACTGGTATCAGCAGAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAAGATGTTGCAACTTACTACTGTCAACAGAGTTNCACTTATGNCTCGGACGGTTGGCC
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heavy chain,
T28938
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For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST61186 Homo
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human primer=M13 Reverse library=Human White blood cells
                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 209)
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Pred. No: 2.95e-120;
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Best Local
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                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 CCAGTGAATGAGTAACCAGAAGTCTTGCAGGATATCTTCATTGAACCTCCAGGCTTCACC
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11 Similarity 71.7%;
134; Conserver'
                                                                                                                                                                                                                                                                                               double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p3773 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haselline,W.A., Fields,C., Fraser,C.M. and Venter,J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
                                                        Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lenon,G., Marra,J.
Parsons,J., Rifkin,L., Rohlfing,T., Scares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. an
                                                                                                                                           Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
(bases 1 to 488)
                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1995)
Unpublished (1995)
                      The WashU-Merck EST
                                                                                                                                                                                                                                     Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                 and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: tdbinfo@tdb.tigr.org
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Pred. No. 4.51e-118;
0; Mismatches 53;
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this EST, please contact the TIGR Database
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                                                            Soares,M., Tan,F.,
son,A., Wohldmann,P. and
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similar to gb:X72467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 TGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAATAAAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.4%;
Local Similarity 66.7%;
Nes 154; Conservation
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                                                                 RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P. J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Frieser, C.M. and Venter, J.C.
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WashU-Werck EST Project
Washington University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1800
Fax: 314 286 1810
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA300732 333 bp mRNA EST13847 Testis tumor Homo sapiens cDNA
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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/clone="161528"
/ 130 c 128 g 12
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Pred. No. 4.51e-118;
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Adams, M.D., Kerlavvge, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
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EST14279
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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/note="Organ: testis; Ve
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Adb_xref="ATCC (inhost):192041"
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67.7%;
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Pred. No. 6.81e-116;
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AII16236 116 bp mRNA
N uc18e08.rl Soares mouse mammary gl
1398374 5' similar to gb:M87789 IC
gb:X67210 M.musculus rearranged in
(MOUSE); mRNA sequence.
AII16236
g3516560
                                                                                                                                                                                                                                 AAGGGACCAAGGTGGAAATCAAA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGGAAAGCCCCTAAGCTCCTGATGTATGGTGCATCCAGTTTTGCAAGGTGGGGTCCCTTC 256
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96026280
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 3018699056
Fax: 3018699423
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ECORI; Site_2: XhoI"
//db_xref="ATCC (inhost):191658"
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Pred. No. 6.81e-116;
1; Mismatches 104;
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                                                                                gland NbMMG Mus musculus cDNA clone IG GAMMA-1 CHAIN C REGION (HUMAN);
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1 (bases 1 to 116)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
Machington University Section 1 Medicinep
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Fax: 314 286 1810
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<pre>embl55 1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_vi genbank107 15:gb_ba1 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov 21:gb_pat 22:gb_ph 23:gb_pl 24:gb_pl 25:gb_pr1 26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy 32:gb_un 33:gb_vi</pre>	Dbase 0; Query 0 567134 segs, 1101898692 bases x 2 Minimum Match 0% Listing first 45 summaries	8-704-178-1 1) from USC 1 ATGGACCTG TACCTGGAC default	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd  nn n.a n.a. database search, using Smith-Waterman algorithm Sat Jan 9 13:21:31 1999; MasPar time 494.95 Seconds 1429.279 Million cell updates/sec output not generated.	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 9.835; Variance 4.583; scale 2.146

Statistics:

Result	Score	Query Match	Length DB	В	ID	Description	Pred. No.	
۳	314	97.8	711 ;	21	I32406	Sequence 1 from patent	6.19e-249	
2	314	97.8	711 3	۳	S39590	N	6.19e-249	
ω	270	84.1	315	21	I51657	Sequence 3 from patent	3.01e-209	
4	270	84.1	315	2	A36642	Sequence 2 from Patent	3.01e-209	
<sub>5</sub>	270	84.1	321 2	8	MMIG013	Mouse hybridoma 2d3 mR	3.01e-209	
S	267	83.2	312 ;	8	S48339	Ig V kappa =anti-idiot	1.51e-206	
7	267	83.2		8	AF056217	Mus musculus monoclona	1.51e-206	
8	266	82.9		28	MUSIGKAAR	Mouse Ig kappa active	1.19e-205	
9	265	82.6		8	MUSIGKVA2A	Mouse hybridoma Ig rea	9.46e-205	
10	262	81.6		28	MUSIGKCNA	Mouse Ig rearranged ka	4.70e-202	
11	262	81.6		21	109200	Sequence 40 from Paten	4.70e-202	
12	262	81.6	477	8	S76823	Ig V kappa ⇒anti-sigma	4.70e-202	
13	261	81.3	321 2	21	127490	Sequence 4 from patent	3.72e-201	

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binant anti-erbB2 immunotoxins containing Pseudomonas exotoxin
Natl. Acad. Sci. U.S.A. 89 (13), 5867-5871 (1992)
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Kpmixttschasgyparfsggsbyvkpggsmkiscktscysftghtmnwvkqs-
KLEIKGSTSGSGKSSEGKGVQLQESGPEVVKPGGSMKISCKTSCYSFTGHTMNWVKQS-
KLEIKGSTSGSGKSSEGKGVQLQESGPEVVKPGSSTAYMELLSLTSEDSAVYYCAR-
HGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCAR-
                                                                                                                                                                                                                                                                                                                                              RVTDWYFDVWGAGTTVTVS"
182 c 190 ģ
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/note="This sequence comes from Fig. 1."
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1. No. 6.19e-249;
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BASE COUNT
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1 (bases 1 to 315);

3 Seemann,G. and Bosslet,K.

Granulocyte-binding antibody constructs, the
Granulocyte-binding antibody constructs, 
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T51657
                1 (bases 1 to 315)
Seemann,G. and Bosslet,K.
Antigranulocyte antibody
Patent: EP 0585570-A 2 09
                                                                                                                    Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi;
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| Similarity 93.3%;
| 294; Conservative
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Pred. No. 3.01e-209;
1; Mismatches 19;
                    dy construct,
09-MAR-1994;
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Other
Other
Other
                                                                                   Meek,K., Hasemann,C., Pollok,B., Alkan,S.S., Lucus, Urbain,J. and Capra,J.D.

Structural characterization of antiidiotypic antibodies.

Structural characterization the germline differently than
                                                                  J. Exp. 1
89094248
                                                                                                                                                         Submitted (09-JAN-1989) K. Meek, Medical School, 5323 Harry Hines
                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; I
                                                                                                                                                                                                                                                 Mus musculus
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Ig kappa light chain;
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Similarity 93.3%;
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/db_xref="taxon:10090"
/cell_type="hybridoma/myeloma"
/2 c 80 g 71 t
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1. .315
          /organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
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/cell_line="Hybridoma 2D3-K"
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Pred. No. 3.01e-209;
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Myomorpha;
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Dallas Texas
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGCAGG 76
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                                                                                                                                                                                                    Mus sp.
Mus sp.
Eukaryotae; i
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S48339
g257749
GenBank staff at the National Library of Medicine created entry [NCBI gibbsq 118382] from the original journal artic This sequence comes from Fig. 5.

Location/Qualifiers
1. .312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289;
                                                                                                Linnenbach, A.J.

Molecular cloning of murine monoclonal anti-idiotypic
J. Immunol. Methods 155 (1), 77-89 (1992)
                                                                                       93017981
                                                                                                                                               1 (bases 1 to 312)
Kasai,Y., Herlyn,D.,
                                                                                                                                                                                                                                                                                                                                          S48339
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llarity 94.8%;
Conservative
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LEIKR"
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/note="variable region"
/product="IG kappa light chain"
<1. .>321
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/note="variable region"
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/note="variable region"
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-anti-idiotypic
                                                                                                                                                                                                  mitochondrial eukaryotes; Metazoa;
Eutheria; Rodentia; Sciurognathi; I
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Pred. No. 3.01e-209;
1; Mismatches 14;
                                                                                                                                                   Sperlagh, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGC 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCC 133
                                                                                                                                                                                                                                                           Mus musculus partial cds. AF056217
                                                          2 (bases 1 to 318)
Sandstrom, P., Johansson, A., Ullen, A., Behravan, G. and Stigbrand, T. Direct Submission
                                                                                                                            Sandstrom,P., Johansson,A., Ullen,A., Behravan,G. and Stigbrand,T. Differences in sequence and affinity between three monoclonal anti-idiotypic antibodies against one anti-placental alkaline
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 318) 1 (bases 1 to 318) 5 and Strom, P., Johansson, A., Ullen, A., Behravan, G. ar
                                         Sweden
                                                 Submitted (30-MAR-1998) Immunology,
                                                                                                    Unpublished
                                                                                                                 phosphatase idiotypic antibody
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                                                                                                                                                                                                                                                                                                 AF056217
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                         Location/Qualifiers
/organism="Mus musculus"
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/translation="VMTQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPW
IVATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPWTFGGGTKLE
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/note="anti-idiotypic Fab;
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/gene="Ig V<down>&kgr;</down>"
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/db_xref="taxon:10095"
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. No. 1.51e-206;
Mismatches 17;
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                                                  Umea
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                                                                                                                                                                sequence
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Query Match 83.2%;
Best Local Similarity 92.5%;
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                                                                                                                                                                                                                                                                                1 (bases 1 to 1370)
Parslow,T.G., Blair,D.L., Murphy,W.J. and Granner,D.K.
Structure of the 5' ends of immunoglobulin genes: A no
                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin-kappa. Mouse 70Z/3 cell DNA.
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C-region; V-region; immunoglobulin light chain;
                                                                                                                                                                           Corrections to the sequence were sent by Dr. Tristram G. Parslow on Dec. 9, 1991.
                                                                                                                                                                                                                                                                                                                                                          Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAAR 1370 bp DNA
Ig kappa active V-region
                                                                                                                                                                                                                                           Natl. Acad. Sci. U.S.A. 81, 2650-2654 (1984)
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/number=1
join(776.
                                         /organism="Mus musculus"
/db_xref="taxon:10090"
<776. .824
/note="Ig kappa chain va
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/translation="DIQLTQSPAILSASPGEKVSMTCRASSSVSYIHWYQQKPGSSPK
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/cell_line="hybridoma"
                                                                                                                                                        Location/Qualifiers
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alkaline phosphatase antibody; variable region"
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                                       kappa chain variable region"
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Pred. No. 1.51e-206;
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                                                                                       Lohman, K.L., Kieber-Emmons, T. and Kennedy, R.C. Molecular characterization and structural modeling of immunoglobulin variable regions from murine monoclonal specific for hepatitis B virus surface antigen Mol. Immunol. 30 (14), 1295-1306 (1993) 94019421
                                                                                                                                                                                                                                                                                        immunoglobulin light chain;
variable region
                                                                                                                                                                                                                                                                                                                                                       Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; N
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1338. .>1369
/note="kappa
a 273 c
              /organism="Mus musculus"
/db_xref="taxon:10090"
101 c 89 g 7
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CRASSSVSYMHWYQQKPGSSPKPWIYATSNLASGVPARFSGSGSGTSYSLTISRVEAE
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1003. .>1337
| note="Ig kappa chain variable
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/db_xref="PID:g196461"
                                                                       Location/Qualifiers
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94.18;
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Myomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 CAAACCCTGGATTTATGCCACATCCAACCTGGCGTCTGGAGTCCCTGCTTCAGTGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 CAGTGGGTCCGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 CAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 CAGGGCCAGTTCAAGTGTAGGTTCCATACACTGGTACCAGCAGAAGCCAGGATCCTCCCC 125
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     282;
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Production of a mouse-human chimeric monoclonal
with potent Fc-dependent biologic activity
J. Immunol. 139, 3521-3526 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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C-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; processed gene.
Mus musculus cDNA to mRNA.
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M17954
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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iu, 02-FEB-1987.
     Conservative
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                                                                                                                                                                /codon_start=1
/product="immunoglobulin kappa-chain"
/product="immunoglobulin kappa-chain"
/db_xref="pID:g466303"
/translation="MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMT
/translation="MDFQVQIFSFLLISASVIIARGQIVLSQSSGTSYSLTISRVEAE
CRASSSYSYMHWQQKRGSSFRFWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAE
                                                                                    /note="V-region end/J-5-region
/organism="Mus musculus"
112 c 93 g 98 t
                                                                                                                                          DAATYYCQQWSFNPPTFGAGTKLELK" 370. .371
                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="2H7"
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                   81.6%;
94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 bp
Score 262; DB 28;
Pred. No. 4.70e-202;
1; Mismatches 15;
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Pred. No. 9.46e-205;
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1 (bases 1 to 403)
Robinson, R.R., Liu,
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Similarity 94.3%;
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1; Mismatches 15;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
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CRASSSVSYIHWYQQKPGSSPKPWILATSNLASGVPARFSGSGSGTSYSLTISRMEAE
DAATYYCQQWSRNLYTFGGGTKLEIKRLMLHQLYPSSHHP"
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/gene="Ig V&kgr;"
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I05923
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Chimeric antibody with specificity to
Patent: Ep 0274394-A2 39 13-JUL-1988;
Location/Qualifiers
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Hoogenboom, H.R.J.M., Baier, M., Jespers, L.S.A.T. and Winter, G.P. Production of chimeric antibodies - a combinatorial approach Patent: US 5565332-A 4 15-OCT-1996;
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/strain="Balb/c"
/db_xref="taxon:10090"
/cell_type="hybridoma"
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91 c 76 g 71
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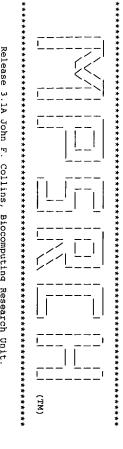
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Jan 9 14:31:15 1999; MasPar time 60.25 Seconds 724.916 Million cell updates/sec Tabular output not generated.

Scoring table: TABLE default
Gap 6

Nmatch

STD :

Dbase 0; Query 0

earched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part33 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 8.055; Variance 4.678; scale 1.722

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

Score	Query Match I	ength DB	ΙĐ	Description	Pred. No.
314	97.8	711 9	Q55180	Sequence encoding the	2.02e-204
314	97.8		T65006	Single-chain anti-erb	2.02e-204
312	97.2		T17728	Anti-erbB2 scFv cDNA.	5.83e-203
264	82.2	384 11	Q65630	Murine variable regio	5.34e-168
262	81.6	318 34	T79900	Anti-Factor IX MAb ch	1.52e-166
262	81.6		T77377	Mouse anti-human Fact	1.52e-166
262	81.6		T79899	Anti-Factor IX MAD BC	1.52e-166
262	81.6		N70972	2H7 VL sequence in wh	
262	81.6		N91147	2H7 Vh sequence.	
262	81.6		T51043	Coding sequence for 1	1.52e-166
262	81.6		T36317	2H7 antibody light ch	1.52e-166
262	81.6		T70869	2H7 light chain varia	1.52e-166
262	81.6		V03927	Mouse 2H7 antibody li	1.52e-166
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Query Match 97.8%; Best Local Similarity 99.7%; Matches 320; Conservative

Score 314; DB 9; Le Pred. No. 2.02e-204; 0; Mismatches 0;

Length 711; 4; 0; Indels

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Gaps

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202 81.6 42.6 40 V18558 MOUSE 2H7 ARTLDODY 1 262 81.6 9208 11 055629 Vector contg. TCAE 8 261 81.6 9208 11 055629 Vector contg. TCAE 8 261 81.3 321 6 039412 Mab32 light chain V-g 257 80.1 387 4 027350 Encodes A5B7 antibody 256 79.8 387 3 020983 Encodes Variable regi 254 79.1 732 24 742508 Murine A5B57 Light ch 252 78.5 435 0 151515 IL-2 chimeric antibody 254 78.2 292 753502 Monoclonal antibody A 251 78.2 292 24 736662 Monoclonal antibody A 251 78.2 292 24 736662 Sequence encoding lig 244 76.0 321 1 N91657 Chimeric antibody Chimeric antibody Chimeric antibody Lig 244 76.0 321 1 N91657 Monoclonal antibody Lig 244 76.0 321 1 N91657 Monoclonal antibody Lig 244 76.0 321 1 N91657 Chimeric antibody Lig 244 76.0 321 1 N91657 Monoclonal antibody C 241 75.1 306 24 736660 Monoclonal antibody C 251 78.2 292 24 736660 Monoclonal antibody C 261 75.2 306 1 045427 Monoclonal antibody C 262 75.2 306 1 045427 Monoclonal antibody C 263 74.5 408 32 736307 V region of the L6 1i 264 76.0 30 74.1 408 31 740860 Monoclonal antibody C 265 81 74.1 408 31 740860 Monoclonal antibody C 266 82 82 82 82 82 82 82 82 82 82 82 82 82
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#### ALIGNMENTS

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Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;	animals given a combination of the 2 Abs, tumours completely regressed after 11 days.	growing tumours were used in a trial of the efficacy of the Abs. In	domain of gp185 erbB-2. Nude mice manipulated to produce rapidly	erbB-2). Abs no. 21 and 23 are directed against the extracellular	engineered to express the human erbB-2 protein on its surface (N/	23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell	The source of human erbB-2 protein for the prodn. of antibodies no.	Example; Fig 7; 37pp; English.	monocional antibodies which recognise different epitopes on	Treatment of malignancies over-expressing ERB-[2 - using at least	P-PSDB; R45442.	WPI; 94-025878/03.	Kasprzyk PG, King CR;	(MOLE-) MOLECULAR ONCOLOGY INC.	30-JUN-1992; US-906555.	21-OCT-1992; U08545.	06-JAN-1994.	WO9400136-A.	/*tag= a	cds 1171	Key Location/Qualifiers	Synthetic.	monoclonal antibody; ss.	Single chain anti-erbBl antibody; cancer therapy; prevention;	Sequence encoding the single chain anti-erbB2 antibody, Ab no.23.	21-JUL-1994 (first entry)	Q55180;	Q55180 standard; cDNA; 711 BP.	3

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                                                                                                  The present cDNA sequence codes for a claimed single-chain antibody, it designated e23(FV), which binds to erbB-2. Monoclonal antibody e23 was generated by immunising mice with NyerbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas in the protein premoving spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide diagnosis of tumour cells which overexpress the erbB-2 gpl85 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours. So Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;
                                                 Query Ma
Best Loc
Matches
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24-DEC-1996.
07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-UUN-1992; US-906555.
11-MAY-1993; US-061092.
""" ARONEX PHARM INC.
                                                                                                                                                                                                                                                                                                 Single chain antibodies specific for erbB-2 protein, gp185 - wit labels or cytotoxin, useful for detection and treatment of tumour cells expressing this protein Example 8: Columns 25-28; 28pp; English.
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Bird RE, Kasprzyk PG,
WPI; 97-064831/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single-chain anti-erbB2 antibody e23(Fv) cDNA.
Single chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma;
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T65006 standard;
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                                                 . Similarity
320; Conser
                                               97.8%;
larity 99.7%;
Conservative
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anti-erbB2 an
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1..711
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                                            Score 314;
Pred. No. 2.
0; Mismatc
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                                                 Mismatches
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                                                             DB 29; 1
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                                                                           Length
                                               Indels
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                                             Gaps
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                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-1995; U10740.
06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
06-JUN-1995; US-468252.
(UABR-) UAB RES FOUND.
Curiel DT, Deshane J;
WPI: 96-171307/17.
P-PSDB; R94020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 42; Page 29-30; 48pp; English.

A nucleac acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a single chain Fv fragment (R94020) that binds a human erbB2 oncoprotein. The anti-erbB2 sFv portion is obtained by PCR using e23scFv plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibody homologue within e.g. an epithelial carcinoma cell. Intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 3
T17728
T17728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibition of proliferation or survival of, esp. malignant cells - by introducing nucleic acid mol. encoding antibody which is expressed and binds, pref. erbB2, protein intraced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy;
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                               tumorigenicity.
Sequence 711
                                                                                                                                                                                                                                                                                                                                                                                                                            expression of the homologue inhibits surface expression of erbB2 and thereby inhibits cell proliferation and cell survival and decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intracellular antibody homologue;
gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncoprotein; erbB2;
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                     120
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                                                                                                                                                                   aggatcctcccccaaaccttggatttataccacatccaacctggcttctggagtccctgc
                                                                       CACAATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCC
                                                                                               cacaatgacttgcagggccaccccaagtgtaagttacatgcactggtatcagcagaagcc
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                                                                                                                                                                                                                                                                                318;
                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  B₽;
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                                                                                                                                                                                                                                                                                                  97.2%;
99.1%;
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                                                                                                                                                                                                                                                                                                                                                                               175 A;
                                                                                                                                                                                                                                                                        Score 312;
Pred. No. 5.
1; Mismatc
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                                                                                                                                                                                                                                                                             Mismatches
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.83e-203;
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                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                       Length 711;
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                                                                                                                                                                                                                                                                                                                                                                               164 T;
                                                                                                                                                                                                                                                                           1;
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121

AGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGC

180

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RESULT RE
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Best Local S
Matches 28
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12-NOV-1993; U10953.
13-NOV-1992; US-978891.
03-NOV-1993; US-149099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSBD; R55214.

Presting B cell lymphoma with chimeric antibody causing rapid depletion of peripheral B cells, als antibodies and hybridomas Disclosure; Fig 4; 101pp; English.

The sequence is the murine variable region light of murine anti-CD20 monoclonal antibody 2BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reffme
WPI; 9
  LT 5
179900 standard;
179900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (first entry)
Murine variable region light chain
B cell lymphoma chimeric antibody;
cell lysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q65630;
01-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAA
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                    cDNA;
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                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 264; DB 11;
Pred. No. 5.34e-168;
1; Mismatches 17;
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CD20;
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RESULT
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AC TY
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DT 27
DE MA
KW 11
KW 11
KW 20
KW 20
KW 20
KW 31
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Thrombosis; therapy; Factor IX
Chimeric antibody; antibody eng
Chimeric Mus muscullus.
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA sequence encodes a mouse-human chimeric antibody light chain (W24532) in which the variable region is derived from mouse anti-human factor IX monoclonal antibody BC2 cDNA (see T79899) and human sequences from the immunoglobulin RF-TS3'CL framework. It was obtained by PCR amplification (see T79897-98) of BC2 cDNA and insertion of the PCR product into F9HZHC 1-3 cDNA (see T77374). Claimed anti-Factor IX chimeric antibodies are useful in the treatment of thrombosis.

Sequence 318 BP; 79 A; 91 C; 78 G; 70 T;
                         26-DEC 1997 (first entry)
Mouse anti-human Factor IX antibody BC2 light chain cDNA.
Thrombosis; therapy; Factor IX; anticoagulant; monoclonal a
humanised antibody; antibody engineering; light chain; CDR;
complementarity determining region; myocardial infarction;
angina; atrial fibrillation; stroke; kidney damage;
pulmonary embolism; deep vein thrombosis; coronary angiopla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blackburn MN, Church WR, Feuers: Nichols AJ, Padlan EA, Patel AH, WPI; 97-385117/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
Blackburn MN, Church WR, Feuerstein GZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-1996;
17-JAN-1996;
shunt; prosthesis;
               disseminated intravascular
                                                                                                                               T77377 standard; cDNA; T7.7377;
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17-JAN-1997;
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                                                                                                                                                                                                                                                                                                                     gccagctcaagtgtaaattacatgcactggtaccagcagaagccaggatcctcccccaaa
                                                                                                                                                                                                        ATAAA 321
                                                                                                                                                                                                                                   atcaa
                                                                                                                                                                                                                                                                               tattactgccagcagtggagtattaacccacggacgttcggtggaggcaccaagctggaa
                                                                                                                                                                                                                                                                                                                                                                                CCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGT
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                                                                                                                                                                                                                                                                TATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                   317
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US-010108.
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                                                                                                                                              321
                                                                                                                                              ВP
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IX; anticoagulant; monoclonal antibody; engineering; light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 262; DB 34;
Pred. No. 1.52e-166;
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               artificial
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            angioplasty;
organ; sepsis;
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                                                                                    antibody;
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RESULT
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AC TT
DT 2:
DT 2:
DE AI
KW TI
KW CI
OS CI
PN WC
PD 2:
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Example 5; Page 64; 150pp; English.

This cDNA sequence encodes the light chain variable region (see C W24520) of mouse anti-human Factor IX monoclonal antibody BC2.

Claimed humanised antibodies (see W24510-18) contain CDRs (see W245104-09) of BC2 heavy and light chains inserted into framework regions of selected human antibody sequences. They have self-limiting neutralising activity, and are useful as anticoagulant agents in treatment of thrombosis associated with myocardial infarction, unstable angina, atrial fibrillation, stroke, renal camage, pulmonary embolism, deep vein thrombosis, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulation, sepsis, or artificial organs, shunts or prostheses (claimed). Also claimed are chimeric antibodies (see T79900), and Fab and F(ab')2 fragments. The claimed antibodies (see T79900), and provide only partial inhibition of coagulation.

Sequence 321 BP; 78 A; 92 C; 79 G; 72 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.

w09726010-A1.

24-JUL-1997.

17-JAN-1997; U00759.

24-OCT-1996; US-029119.

24-OCT-1996; US-029119.

(SMIK) SMITHKLINE BEECHAM CORP.

(UVVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

Blackburn MN, Church WR, Feuerstein GZ, GRONICHOLS AJ, Padlan EA, Patel AH, Sylvester |

wPT; 97-385117/35.
27-DEC-1997 (first entry)
Anti-Factor IX MAb BC2 light chain PCR product.
Thrombosis; therapy; Factor IX; anticoagulant; n
chimeric antibody; antibody engineering; light c
Chimeric Mus musculus.
Chimeric synthetic.
W09725010-A1.
                                                                                                             T79899 standard;
T79899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
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                                                                                                                                                                                                                                                                                                                                             ATAAA
                                                                                                                                                                                                        atcaa 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.6%;
l Similarity 93.4%;
285; Conservation
                                                                                                                                                                               321
                                                                                                                         cDNA; 335
                                                                                                                         ВP
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tel AH, Sylvester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e 262; DB 34; I
. No. 1.52e-166;
Mismatches 18;
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er DR;
                                                      chain;
                                                                  monoclonal antibody;
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                   09-APR-1991 (first entry)
2H7 VL sequence in which the VK
Chimeric antibody; Anti-cancer
Key Location/Qualif
                                                                                                                                                                                                                                                                                                                                                                                                                         N70972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VL region. The PCR product was ligated into ScaI, NarI-digested F9HZHC 1-3 (see T77374) and digested with ScaI, NarI to produce a mouse-human chimeric light chain F9CHLC (see T79900, W24532). Claimed anti-Pactor IX chimeric antibodies are useful in the treatment of thrombosis.

Sequence 335 BP; 80 A; 97 C; 85 G; 73 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-1997; US-0759.
24-OCT-1996; US-029119.
17-JAN-1996; US-010108.
17-JAN-1996; US-010108.
17-JAN-1996; US-010108.
17-JAN-1996; US-010108.
18-JAN-1996; US-010108.
18-JAN-1996; US-010108.
18-JAN-1996; US-010108.
18-JAN-1997; US-010108.
18-JAN-1996; US-010108.
18-JAN-1997; US-0108.
18-JAN-1997; US-01
                                                                         cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This CDNA sequence was obtained by PCR amplification (see T79897 and T79898) of the light chain variable region (see also T77377) of mouse anti-human factor IX monoclonal antibody BC2 cDNA. The amplification resulted in the addition of Scal, Narl ends to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nichols AJ, Padla
WPI; 97-385117/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gccagctcaagtgtaaattacatgcactggtaccagcagaagccaggatcctcccccaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; cDNA; 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Page 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.6%;
llarity 93.4%;
Conservative
                                                                 /*tag= c
/label=CDR1
166..210
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139..165
                  /*tag= d
/label=FR2
                                                                                                                                                                                                                   67..138
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                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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Pred. No. 1.52e-166;

    Mismatches

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N91147 standar
AC N91147;
DT 06-JUL-1990 (fi.
DE 2H7 Vh sequence.
KW Antibodies; pass*.
OS Synthetic.
'H Key
cds
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Best Local Similarity
Matches 282; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                      The patentors claim a chimeric antibody molecule comprising 2 lig chains and 2 heavy chains, each comprising a constant human region and a variable non-human region. Coding sequences for the Ig chains are also claimed. The invention provides consensus sequences of light and heavy chain J regions useful in the design of oligonucleotides (UIGS) for use as primers or probes for cloning immunoglobulinlight or heavy chain mRNAs or genes. Depending on nature of design of a particular UIC, it may be capable of hybridizing to all Ig mRNAs or genes containing a single specific sequence. UIG denotes universal immunoglobulin gene. Sequence 403 BP; 100 A; 112 C; 93 G; 98 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1985; US-793980.
(ITGE-) INT GENETIC ENG INC.
(ROBI/) ROIBINSON R R.
ROBINSON RR, Liu AY, HOTWITZ
WPI: 87-136004/19.
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Example; Fig 22; 126pp;
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                                                                                                                                                 tattactgccagcagtggagttttaacccacccacgttcggtgctgggaccaagctgga
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llarity 94.3%;
Conservative
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232..327
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/label=CDR3
355..403
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/label=FR4
349..403
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328..354
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/label=JK5
        Location/Qualifiers 20..403
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                                         immunisation;
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d. No. 1.52e-166;
Mismatches 15;
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Best Local s
Matches 28
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9-FEB-1988; 02514.
24-UUL-1988; 02514.
24-UUL-1987; US-077528.
(ITGE-) Int Genetic Eng Inc.
Robinson RR, Liu AY, Horwitz
WPI: 89-063144/08.
P-PSDB; P94778.
Polynucleotide(s) encoding In
   US5576195-A.
19-NOV-1996.
01-NOV-1985.
01-NOV-1985.
27-OCT-1986.
24-JUL-1987.
11-ZAN-1988.
29-MAR-1990.
09-DEC-1993.
09-DEC-1993.
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T51043; T51043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; Ig;
myeloma cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence, derived from M13 subclones of gene fragments, carries the variable region of chimeric immunoglobulin sequence. The antibodies useful in passive immunisation avoiding negative reactions. They are also useful in assaying and in vitro imaging.

Sequence 403 BP; 100 A; 112 C; 93 G; 98 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; 7pp; English Sequence, derived from M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used for efficient prodn. class switched antibodies.
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793980.

WS-793980.

WO-U02269.

US-077528.

US-142039.

US-501092.

US-987555.

US-987555.

US-920671.

US-357234.
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320..352
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Horwitz
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                                                                                                                                                                                                                                                                                                                                                               light chain
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Pred. No. 1.52e-166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the coding sequence for the light chain variable region of the 2H7 mouse monoclonal antibody. The 2H7 antibody recognises the human B-cell surface antigen Bp35, which plays a role in B-cell cativation. This sequence was used in a human-mouse chimeric antibody with human B-cell antigen specificity, that was produced using the method of the invention. The method of the invention is for the production of a protein in a Gram-negative bacterium. The method improves on current cetchniques, by using a vector including DNA encoding the pectate lyase continuously sequence (see T51034), attached to the sequence encoding the production. The method is especially used to make continuously contains (1g), particularly those with a human constant region, suitable for passive immunisation (without risk of serum sickness or canaphylaxis) or for in vivo/in vitro diagnosis and imaging. The Ig may calso be used therapeutically, optionally coupled to toxins, etc.

CC Alternatively the protein to be produced is the sweetener thaumatin. The presence of this signal sequence means that the protein is exported from the cytoplasm and can be recovered from the culture medium or periplasm, in active and correctly folded form. The method allows the class of any cantibody to be switched, e.g. most human-human Ig are of M class, easily creduced and aggregated, and these can now be changed to G, A or E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                    T36317 standard; T36317;
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P-PSDB; W10243.

Improved prodn. of protein in Gram -ve b sequence - from pectate lyase to ensure the cytoplasm, essp. for prodn. of antibo Example 4; Fig 22; 86pp; English.
US5595898-A.
21-JAN-1997.
                                                                                       mat_peptide
                                                                                                                                             signal_peptide
                                                                                                                                                                                                                                        therapy; variable
                                                                                                                                                                                                                                                                                                21-OCT-1997 (first entry)
2H7 antibody light chain variable region cDNA.
Immunoglobulin G; IgG; light chain; recombinant
antibody; passive immunisation; serum sickness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                          immunoassay;
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                                                                                                                                                                                                        spp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tattactgccagcagtggagttttaaccccaccgttcggtgctgggaccaagctgga 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999tct999acctcttactctcaccaatcagcagagtggaggctgaagatgctgccact 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGCAGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGTCCAAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 94.3%;
282; Conservative
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                                                                                                                                                                                                                                                                    in G: IgG; light chain; recombinant production;
ssive immunisation; serum sickness; anaphylactic
imaging; reagent; complement mediated lysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                 /*tag= a
109..426
                                                                                                                                                   43..108
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA;
                                                                                                                                                                                                                                        region;
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                                                                                                                                                                                                                                           SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 262; DB 30; Pred. No. 1.52e-166; 1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gram -ve bacteria using signal to ensure transport of protein of antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 T;
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RESULT
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AC TTO
AC TTO
DT 04
DE 24
CE 24
CE 24
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CE 26
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CE 27

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PT dicistronic transcription unit with pectate lysse signal sequences PS Example; Fig 22; 95pp; English.

CC The present sequence encodes the light chain variable region of CC the 2H7 antibody. The 2H7 cDNA was used in the preparation of CC molecule comprises 2 DNA sequences encoding an Ig fragment. The DNA CC molecule comprises 2 DNA sequences encoding 2 pectate lysse secretion signal sequences respectively linked to a DNA sequence CC encoding an Ig Fd molecule or Ig light chain, operably linked to a Single prokaryotic promoter so as to form a dicistronic transcription unit, provided that the Ig fragment can bind an antigen and is produced and secreted by an E. coli host cell when CC the nucleic acid molecule is expressed in the host cell when CC manifyen and independent encourage of the production of recombinant antibodies, which can be used for passive immunisation CC without negative immune reactions (e.g. serum sickness and anaphylactic shock), in labelled forms as immunoassay or imaging CC reagents, in complement mediated lysis and for therapeutic purposes when coupled to a toxin or other therapeutic agent.

So Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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29-MAR-1990;
01-NOV-1985;
27-OCT-1986;
24-JUL-1987;
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08-DEC-1992;
18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                        T70869;
04-SEP-1997 (first entry)
2H7 light chain variable s
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Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
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Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Better M, Liu AY, Robins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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ilarity 94.3%;
Conservative
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US-501092.
US-793980.
WO-U02269.
US-077528.
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US-987555.
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                                                                                                                                                                                                                                                                                                                                                            sequence.
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Pred. No. 1.52e-166;
1; Mismatches 15;
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Antibody engineering; heavy chain; light chain; chimaeric antibo passive immunisation; diagnosis; hybridoma; monoclonal antibody; 247; B-cell antigen; Bp35; ss.

chain; light chain; chimaeric antibody;

mat\_peptide signal\_peptide

/\*tag= a

/\*tag= b

Location/Qualifiers 43..240

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RESULT VV
AC VV
AC VI
DT 0:
DT 0:
MM MM
KW in
KW
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Best Local S
Matches 28
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01-NOV-1985; US-793980.

27-OCT-1986; WO-U02269.

24-JUL-1987; US-077528.

11-JAN-1988; US-142039.

29-MAR-1990; US-510192.

17-APR-1992; US-870404.

29-APR-1994; US-235225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secretable immunoglobulin heavy and light chain fragments - capabl of assembling into chimeric antibodies, useful for e.g. passive immunisation, diagnosis, etc example 4; Fig 22; 96pp; English.

A cDNA clone (770869) codes for the light chain variable region (W16344) of the 2H7 mouse monoclonal antibody, which recognises human B-cell surface antigen B935. The sequence was isolated from a 2H7 cell line cDNA library by PCR amplification. The 2H7 heavy chain variable sequence (T60868) has also been isolated. The sequences have been used to construct a human-mouse chimaeric antibody with specificity for the human B-cell antigen. Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;
                                                                                                                                                                                         01-JUN-1998 (first entry)
Mouse 2H7 antibody light chain variable region cDNA.
Mouse; murine; light chain; variable region;
immunoglobulin fragment production; Ig fragment production; of the production of the p
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08-APR-1997
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                                                                                                        sig_peptide
                                                                                                                                                                          Mus sp.
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97-225473/20.
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Similarity 94.38;
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109..426
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/note= "Jk5 sequence
406.420
/*tag= d
                                                                                                    Location/Qualifiers 43..108
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Pred. No. 1.52e-166;
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                                                                                                                                                                                                        g fragment production;
surface antigen; ss.
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    cencoling: (a) pectate lyase secretion signal sequence operably can ly fd molecule; and (b) pectate lyase secretion signal sequence operably inked to a DNA sequence encoding at least the variable region of coperably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a single prokaryotic promoter to form a dicistronic crasscription unit. The method is used to produce chimeric Fab conclecules, e.g. derived from murine monoclonal antibody 2H7 raised accomptant human B-cell surface antigen. The invention provides a convel approach for producing genetically engineered antibodies of desired variable region specificity and constant region croperties. The cloned Ig gene products can be produced by expression in genetically engineered organisms. The application of specific Ig chains in various organisms provides an effective concordinal antibodies. The invention also provides a solution to the problem of class switching antibody molecules.

Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;
                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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27-OCT-1986;
24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
25-MAY-1995;
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02-DEC-1997.
25-MAY-1995;
29-MAR-1990;
LT 14
V18558
V18558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transformed with dicistronic expression cassette
Example IV; Fig 22; 98pp; English.
The present sequence was used in the development of a novel method for the production of an immunoglobulin (Ig) fragment capable of binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the Ig fragment, under conditions so that the Ig fragment is produced and secreted. The nucleic acid molecule comprises DNA sequences
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Better M, Horwitz AH, Lei
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                                                                                                                                                                                                                                                                         gccagctcaagtgtaagttacatgcactggtaccagcagaagccaggatcctcccccaaa
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                                                                                                                                                                                                                                                                                                                      CCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                  282;
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US-501092.
US-793980.
WO-U02269.
WO-U7528.
US-142039.
US-98755.
US-299085.
US-450731.
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                                                                                                                                                                                                                                                                                                                                                                              Score 262; DB 40;
Pred. No. 1.52e-166;
1; Mismatches 15;
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                                                                                                                                                                                                                                                                                                 PT DNA encoding secretable immunoglobulin fragments - comprising at PT DNA encoding secretable regions of light or heavy chains PS Example IV; Fig 22; 98pp; English.

CC The present sequence was used in the development of a novel method CC for the production of an immunoglobulin (Ig) fragment capable of CC binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the CC Ig fragment, under conditions so that the Ig fragment is produced CC and secreted. The nucleic acid molecule comprises DNA sequences CC encoding: (a) pectate lyase secretion signal sequence operably CC linked to a DNA sequence encoding at least the variable region of CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence coperably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked CC to a single prokaryotic promoter to form a dicistronic CC transcription unit. The method is used to produce chimeric Fab CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised against human B-cell surface antigen. The invention provides a cc compression in genetically engineered antibodies of CC desired variable region specificity and constant region produced by expression in genetically engineered antibodies of CC expression in genetically engineered antibodies of CC expression in entibodies, recombinant DNA cloning and production of CC specific Ig chains in various organisms provides an effective consolonal antibodies. The invention also provides a solution to CC the problem of class switching antibody molecules.

Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;
                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                Matches
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Mouse 2H7 ar
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Better M, Horwitz AH, Lei
                                     137
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98-051492/05.
                                999tct999acctcttactctctcacaatcagcagagtggaggctgaagatgctgcact
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WO-U02269.
US-142039.
US-987555.
US-299085.
US-467140.
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109..426
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94.3%;
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                                                                                                                                                                                                                             Score 262; DB 40; I
Pred. No. 1.52e-166;
1; Mismatches 15;
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                                                                                                                                                                                                                                                             Length 426;
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RESULT PROCESSION OF THE PROCE
                                                                                                                                                         If fragment, under conditions so that the Ig fragment is produced and secreted. The nucleic acid molecule comprises DNA sequences conditions in the sequence operably continued to a DNA sequence encoding at least the variable region of an Ig Fd molecule; and (b) pectate lyase secretion signal sequence coperably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a DNA sequence encoding at least the variable composed to a single prokaryotic promoter to form a dicistronic consist the contract of the method is used to produce chimeric Fab composed and the sequence monoclonal antibodies of composed approach for producing genetically engineered antibodies of composed approach for producing genetically engineered antibodies of composed approach for producing genetically engineered organisms. The application of composed spring in genetically engineered organisms. The application of specific Ig chains in various organisms provides an effective composition for the efficient large scale production of human continues of composition of the efficient large scale production of human continues of composition of the efficient large scale productes.
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24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
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Example IV; Fig 22; 98pp; English.

Example IV; Fig 22; 98pp; English.

The present sequence was used in the development of a novel method for the production of an immunoglobulin (Ig) fragment capable of binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the lig fragment, under conditions so that the Ig fragment is produced
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V18594;
05-JUN-1998 (fi
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01-NOV-1985;
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uence 426 BP; 100 A; 135 C; 93 G;
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WS-793980.
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US-299085.
US-450731.
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Score 262; DB 40;
Pred. No. 1.52e-166;
1; Mismatches 15;
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Gaps
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В

122 cccagtctccagcaatcctgtctgcatctccaggggagaaggt-cacaatgacttgcagg 180

Search completed: Sat Jan 9 14:32:20 1999 Job time : 65 secs.

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Nmatch STD : Dbase 0; Query 0

2275026 seqs, 895388244 bases x 2

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

emb1-est55
1:em\_est1 2:em\_gss1 3:em\_gss2 4:em\_gss3
genbank-est107
5:gb\_est1 6:gb\_est10 7:gb\_est11 8:gb\_est12 9:gb\_est13
10:gb\_est1 41:gb\_est15 12:gb\_est16 13:gb\_est17
14:gb\_est14 11:gb\_est15 16:gb\_est16 17:gb\_est20
18:gb\_est12 19:gb\_est3 20:gb\_est4 21:gb\_est5 22:gb\_est6
23:gb\_est7 24:gb\_est8 25:gb\_est9 26:gb\_gss1 27:gb\_gss2
28:gb\_gss3 29:gb\_gss4

Statistics: Mean 9.931; Variance 1.885; scale 5.267

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

11110987654321	Result No.
232 179 91 84 81 80 79 79 79 78 78	Score
72 22 22 24 3. 4. 4. 4. 5. 6. 6. 6. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7.	Query Match
396 3454 3454 3454 3454 3468 3468 3468 3468 3468 3468 3468 346	% Query Match Length
11 12 12 14 15 16 16 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18	BB
AA691311 AA592800 AA710291 AA318377 T27593 H25625 AA921173 AA300732 AA300732 AA301347 AA295941 AA295993 AA295993	ID
vs14f01.rl Barstead mo vo25g11.rl Barstead mo vo25g11.rl Barstead mo vt53a04.rl Barstead mo EST20620 Spleen I Homo EST20623 Homo sapiens y148g05.rl Homo sapien y54b07.rl Stratagene EST13847 Testis tumor EST10479 Testis tumor EST101479 Testis tumor EST101471 Pancreas tum EST100471 Pancreas tum ST100471 Pancreas tum	Description
0.00e+00 0.00e+00 2.27e-131 3.89e-117 4.41e-111 4.53e-109 4.61e-107 4.61e-107 4.66e-105 4.66e-105 4.67e-103	Pred. No.

3.7 276 13 AA869306 Vq50c10.r1 Barstead 3.7 403 25 AA34548 EST51505 Gall bladed 3.4 352 24 AA301261 SST51505 Gall bladed 3.1 463 16 R69332 Yy82d09.r1 Homo sapi 3.1 470 19 H62115 Yy82d09.r1 Homo sapi 3.1 470 12 AA35086 EST3447 Esophagus t 2.4 442 10 AA405415 zu56d02.r1 Soares ov 1.8 328 24 AA318628 EST20808 Spleen I Hom 1.8 503 5 R28232 Yh57e08.r1 Homo sapi 1.5 339 11 AA710249 tt49e01.r1 Barstead 1.5 339 11 AA710249 Yt49e01.r1 Barstead 1.5 339 11 AA710249 Y122f09.r1 Homo sapi 1.5 339 11 AA70249 Y122f09.r1 Homo sapi 1.5 346 16 R64993 Y122f09.r1 Homo sapi 1.6 382 24 AA300891 EST100987 Pancreas t tumo 1.8 363 24 AA300891 EST100987 Pancreas t tumo 1.8 363 24 AA300891 EST3764 Testis tumo 1.8 363 24 AA300651 EST3764 Testis tumo 1.9 363 25 AA36149 EST3104 r1 Homo sapi 1.9 397 5 R46878 YP22b04.r1 Homo sapi 1.9 397 5 AA36149 EST71040 T-cell lymp 1.9 363 26 AA307405 EST71040 T-cell lymp 1.9 363 26 AA36578 EST711.r1 Soares ov 1.9 36 24 AA300582 EST33647 Testis tumo 1.9 36 36 37 AA465678 Zw27f11.r1 Soares ov 1.9 36 36 37 AA465678 Zw27f11.r1 Soares ov 1.9 346 24 AA300582 EST33647 Testis tumo	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	
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	13427 Testis tumor	Ofll.rl Soares ova	3c09.rl Soares ova	7fll.rl Soares ova	99871 Homo sap	78511 Pancreas	71040 T-cell 1	4h03.rl Homo sap	5c03.rl Homo sap	2b04.rl Homo sap	30547 Colon I	13764 Testis tumo	8cl2.rl Soares ov	2h11.r1 Homo sapi	Da03.rl Soares π	100987 Pancreas	14031 Testis tumc	8g06.rl Soares ova	2f09.rl Homo sapie	5d05.rl Homo sapie	59384 Homo sapien	e01.rl Barstead	7e08.rl Homo sap	ST20808 Spleen I F	6d02.rl Soares o	39457 Esophagus	OhO1.rl Homo sapi	2d09.rl Homo sapie	14181 Testis tumo	ST51505 Gall bladde	q50c10.r1 Barstead	COURT OF CALCE

## ALIGNMENTS

FEATURES Source		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION NID KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS DEFINITION
Seq primer: -28m13 rev2 ET from Amersham. Location/Qualifiers 1. 396 /organism="Mus musculus" /strain="FVB/N" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified	Contact: Marra M./Mouse EST project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGT:610473	Gelsel.S., Kucaba,T., Lacy,M., Te,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. The WashU-HHMI Mouse EST Project Unpublished (1996)	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 396) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,	AA691311 9269247 EST. house mouse. Mus musculus	AA691311 396 bp mRNA EST 16-DEC-1997 vs14f01.rl Barstead mouse irradiated colon MPLRB7 Mus musculus CDNA clone 1138201 5' similar to 9b:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                          Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Euther Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 344)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA592800 344 bp mRNA EST 17-SEP-1997 vo25g11.rl Barstead mouse irradiated colon MPLRB7 Mus musculus clone 1050980 5' similar to 9b:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                      Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                               Waterston, R.
The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                                                                                                                                                          g2406463
                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                       mouseest@watson.wustl.edu
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/lab_host="DH10B"
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89.6%;
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                                        Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 345)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                             vt53a04.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1166766 5' similar to gb:X02484_rnal IG KAPPA CHAIN PRECURSOR V-IV REGION (HUMAN); gb:J00560 mouse ig kappa mrna from mopc2l & other myeloma mrna 3' (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq p
                                                                                                                                                                                                                                                              AA710291
              The WashU-HHMI Mouse 
Unpublished (1996)
                                                                                                                                                                                                                                            g2720209
                                                                                                                                                                                                                                                                                                                                                    AA710291
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larity 83.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 3']; double-stranded cDNA was ligated to Eco RI adaptors [ANTICGOATCCTTG], digested with Not I and into the Not I and Eco RI sites of the modified powertor. Library constructed by Bob Barstead." /db_xref="taxon:10090" /clone="105980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>^</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
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91 c
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Pred. No. 0.00e+00;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                CAGAGTATTTCTGTCAGCAATATAACAGCTTTCCGTACACGTTCGGAGGGGGGGACCAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGCCACCCCAA-GTGTA-AGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCC
                                  AA318377 335 bp mRNA EST 19-APR-1997 EST20620 Spleen I Homo sapiens cDNA 5' end similar to similar immunoglobulin kappa light chain, V region, anti-thyroglobulin (GB:X79786), mRNA sequence.

AA318377 g1970863 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M./Mouse EST project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800 Fax: 314 286 1810
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer: -28ml3 rev2 ET from h quality sequence stop: 140.
Location/Qualifiers
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/dev_stage="8 weeks"
/lab_host="DH10B"
81 c 88 g 81 t
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/db xref="taxon:10090"

/clone="1166766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from 8 week old mouse. Col irradiation with 1400 Gys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 91; DB 11; I
Pred. No. 2.27e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1st strand cDNA was primed
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Best Local :
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                                                                                                                              156 TTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTTGCAACTTACTACTGTCAACAG 215
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                                               216 AGTTCCAGTAGCCCTTGGACGTTCGGCCAAGGGNCCAAGGTGGCAATCAA 265
                                                                                                     212 TACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAG
                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                    92 AGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAACCTTGGATTTATACC 151
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                                                                                                                                                                                                             ACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGTGGGTCTGGGACCTCT
                                                                                                                                                                                                                                                                                                                                                                       AGCTATTTACATTGGTATCAGCACAAACCAGGTAAAGCCCCCTAAACTCCTGATCTATGNT 95
TGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAATAAA 321
                                                                                                                                                                                                                                                               ACATCCACTTTGCAAAGTGGGGTCCCCATCAAGGTTCAGTGGCACTGGGATCTGGGACAGAT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
White, O., Sutton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
155; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
For clone availability, additional sequence and exinformation related to this EST, please check the Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: spleen; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):119058"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Spleen I"
/sex="male"
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Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of CDNA Sequence
                                                                                                                                             TCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGC
                                                                                                                                                                                              AAGGTTCAGTGGCTCTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACC
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EST100653 Homo sapiens
The chain, V region
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Other_ESTs: THC24356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Date of the trick of the trick
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                                                                                                                                                                                                                                                   152 ACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGTGGGTCTGGGACCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-Merck EST Project
Washington University Sch
4444 Forest Park Parkway,
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yl48g05.rl Homo sapiens cDNA clone 161528 5' similar
IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);.
H25625
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hiltman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
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130 c 128 g 12
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                              141
                                                                                                                                                77
                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                               GCCATCTCAAGTATAAGTAACATGTACTGCTACCAGCAGAAGCCAGGATCCTCC 194
                                                                                                                                                                                                                            CCCAGTCTCCAGCAATCATGTCTACATCTCCAGGGCAGAAAGT-CACCATGACCTGCAGT 140
                                                                                                                                               GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCC
                                                                                                                                                                                                            CCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGCAGG
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EST13847 Testis tumor Homo sapiens cDNA 5' end similar to similar to immunoglobulin Kappa light chain (GB:S49006), mRNA sequence AA300732 g1953300 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vy54b07.rl Stratagene mouse lung 937302 Mus musculus cDNA clone 1299253 5' similar to gb:x67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 194)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuc Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project Washb-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lc Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g3067952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                          Similarity
99; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:680301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                       24.6%;
larity 86.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="lung"
/dev_stage="6-8 month old"
/lab_host="SOLR (kanamycin resistant)"
54 c 39 g 47 t
                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Stratagene mouse
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                     Score 79; DB 14; L
Pred. No. 4.61e-107;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                  lung
                                                                                                                                                                                                                                                                                                     Length 194;
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BASE COUNT
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                          103
                                                                                                                                             163
                   283
                                                                                                                                                                           63
                   CCCACCCACGTTCGGAGGGGGGTCCAAGCTGGAAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96026280
Other_ESTs: THC87411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                    24.6%;
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, J., Wal, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
AL Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                  3 CTGGTATCAGCAGAAACCAGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTT 62
CCCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 221
                                                                        AGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCGTAG
                                                                                                                                        CATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTT 182
                                                                                                                                                                                                                        KGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGTGGGGTCTGGGACCTCTTACTCTCTCAC
                                                                                                                                                                                                                                                                                            GCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCAC 122
                                                                                                                                                                                                                                                                                                                                                                    CTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCT
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: testis; Vector: pBluescript SK-;
ECORI, Site_2: XhOI"
/db_xref="ATCC (inhost):192041"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
<1. .>333
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Pred. No.
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No. 4.61e-107;
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                                                   137
     6<u>4</u>
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                                                                                                                      GACATTCAGATGACCCAGTCTCCCATCCCTGTCTGCCATCTGTGGGAGACAGAGT-CAC 136
AATGACTTGCAGGGCCACCC--CAAGTGTA-AGTTACATGCACTGGTATCAGCAGAAGCC 120
                                         CATCACTTGCCGGGCTGGGCAGCACTTAACACCTATTTAAATTGGTATCAACAGAAACC 196
                                                                                               GACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACAC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
AA301347
g1953680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M.D.,
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Vertebrata;
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                                                                                                                                                                                                                           Similarity
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ams,M.D., Kerlavage,A.R., Fleischmann,R.D.,
                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: testis; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):191658"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Testis tumor"
                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                        24.6%;
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                                                                                                                                                                                            Score 79; DB 24; L
Pred. No. 4.61e-107;
1; Mismatches 104;
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                                                                                                                                                                                                 Indels
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RESULT
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                                                                                                                                                                      FEATURES
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ORGANISM
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MEDLINE
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                                                                                                                                            source
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Woreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Frister, C.M. and Venter, J.C.
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                                                                                                                                                                                                                  For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                           Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                             Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                         Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
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/note="Organ: thymus; Vector: p
EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):191388"
/db_xref="taxon:9606"
                                                                                                                                                                Location/Qualifiers
                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                     Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu.C., Yu.G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCCGGTGGGTCTGGGACCTCTTACTCTCAC
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                   Email: arkerlavetigr.org
For Clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human
Index (http://שישי.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                              Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                           9712 Medical Center Drive,
                                                                                                                                                                                      Bioinformatics
                                                                                                                                                                                                                            Other_ESTs: THC168243
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Bult, C.J., 1
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Similarity 66.7%;
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1 69 c 65 g
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tumor I Homo sapiens cDNA 5' end similar to
lobulin kappa, variable region (GB:Y00640), mRNA
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                                                                                                                                         Rockville,
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4.66e-105;
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                  Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wal.C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehn,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kosch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Ersser,C.M. and Venter,J.C., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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ECORI, Site_2: XhO!"
/db_xref="ATCC (inhost):190705"
/db_xref="taxon:9606"
/clone_lib="Pancreas tumor I"
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Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ost
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H(
1 (bases 1 to 210)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins
                                                                                                                                   1 Similarity
175; Conse:
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/db_xref="ATCC (inhost):190766"
/db_xref="taxon:9606"
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                                                                    Hillier, L., Allen, M., Bowles, L., Dubuque, T., Ge: Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., White, Y., Wylle, T., Waterston, R. and Wilson, R. WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                 AA479857 242 bp
zu35b05.rl Soares ovary
5' similar to gb:X06764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts:
High quality sequence stops: 1
           Washington University Sch
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.
Location/Qualifiers
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                                               Contact: Wilson
                                                                                                                                                                                             Homo
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Parsons,J., Rifkin,L., Rohlfing,T., Soar
                                                                                                                                                                                                                                                                                                                        (HUMAN);, mRNA
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/clone="155332"
56 c 46 g 5
                                                                                                                                                                                                         mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Pred. No. 4.64e-101;
1; Mismatches 60:
           School of Medicine way, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                      IG KAPPA CHAIN PRECURSOR
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             Louis,
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                                                                                                                                                                                                                                                                                                                     AA869306
g2964751
EST.
                                                                                                                                                                                                                                                                                                                                                                            AA869306 276 bp mRNA EST 16-MAR-1998 vq50c10.rl Barstead bowel MFLBB9 Mus musculus cDNA clone 1097682 similar to gb:x67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE); mRNA sequence.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 276)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuq
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
                                                                             Unpublished (1996)
                                                                                                Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                  house mouse.
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66 c 69 g
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/clone="739953"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares ovary tumor NbHOT"
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Pred. No. 4.64e-101;
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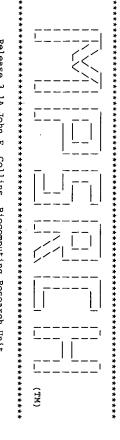
Search completed: Sat Job time: 466 secs.

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                                                                                              180
 136
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                               ACTATGGATTTATTACACATCCAAC-TGGCT-CTGGAGTCC
                                                                                            GGC-AGCTCAAGTGTAAATTACATGTACTGGTACCAGCAGAAGTCAGATGCCTCCCC-AA 237
                                                                                                                             ACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGCAG 75
                                                              GGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAA 135
ACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCC
                                                                                                                                                                                            135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector to vector length is 724
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:603914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Barstead
                                                                                                                                                                                                                                                                                                     /clone_lib="Barstead
/tissue_type="bowel"
/dev_stage="8 weeks"
                                                                                                                                                                                                                                                                     /lab_host="DH10B"
63 c 59 g
                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="1097682"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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Pred. No. 4.64e-101;
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 176
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Jan 9 15:15:33 1999; MasPar time 533.48 Seconds 1437.582 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-08-704-178-1 (364-711) from US08704178.seq (3 of 348 4)

364 TGTGCAGCTGCAGGAGTCAG.......GGGACCACGGTCACCGTCTC ACACGTCGACGTCCTCAGTC...........CCCTGGTGCCAGTGGCAGAG 711

Scoring table: TABLE default Gap 6

Searched: 567134 seqs, 1101898692 bases x 2 Nmatch

STD :

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

emb155
1:em\_ba 2:em\_fun 3:em\_htg 4:em\_hum1 5:em\_hum2 6:em\_in
7:em\_on 8:em\_or 9:em\_ov 10:em\_pat 11:em\_ph 12:em\_pl
13:em\_ro 14:em\_vi
genbank107
15:gb\_ba1 16:gb\_ba2 17:gb\_htg 18:gb\_in 19:gb\_om 20:gb\_ov
21:gb\_pat 22:gb\_ph 23:gb\_pl1 24:gb\_pl2 25:gb\_pr1
26:gb\_pr2 27:gb\_pr3 28:gb\_ro 29:gb\_st 30:gb\_sts 31:gb\_sy
32:gb\_un 33:gb\_vi

Statistics: Mean 9.880; Variance 4.986; scale 1.981

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result
Score
% Query Match
% Query Match Length DB
DB
ID
Description
Pred. No.

В

543 CCAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACAT 602

2.4 366 28 AF081541 MUSHA4 A A A A A A A A A A A A A A A A A A	45	44	43	42	41	40	39	38	37	36	ដូ	34	ဌဌ	32	31	30	29	28	27	26	25	24 .	23	22	21	20	19	18	17	16	15	14
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ω	ACTACAA 543	ATACTA	CAATGGTG	ATCCTTAC	GGAAAGAACCTTGAGTGGACTTGATTAATCCTTACAATGGTGATACTAACTA	STEGATTO	CTTGAG	TGGAAAGAACCTTGAGTGGATTGGACTTATTAATCCTTACAATGGTGATACTAACTA	484	Qy
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ω	AGAGCCA 483	TGAAGC.	JAACTGGG	ACACCAT	:TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCC	TACTCA	FICIGGI	CTGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCA	424	Qy
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ω	AGATATC 423	CAATGA	rggaggtt	TGAAGCC	GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATV	TCAGGAC	CAGGAG	TGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATC	364	Qy
2	AGATATC 422	CAATGA	rggaggtt	TGAAGCC	CTGAGGTGG	TCAGGAG	CAGGAG	TGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATC	363	밁
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/db_xref="pld:q251114"
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GACTCTGCAGTCTATTACTGTGCAAGAGAGTGGTTACTAC-GGTACTTCGATGTCTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Igarashi, K., Asai, K., Kaneda, M., Umeda, M. and Inoue, K. Specific binding of a synthetic peptide derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus.
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larity 90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 is in conflict with the conceptual translation; mismatch(35[K->N])"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="anti-phosphatidylserine monclonal heavy chain variable region" | yene="Ig VH"
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                                                TAAGGCTA--TGGACTACTGGGGCCCAAGGGACCACGGTCACCGTCTC 347
                                                                                                 GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGAGGGTTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-APR-1995) Lin Xu, Institute of Biophys Sinica, Dept. of Protein Engineering, 15 Datum Road, District, Beijing 100101, Peoples Republic of China Location/Qualifiers
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/db_xref="taxon:10090"
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S74055 355 bp mRNA IgG VH IIA-IgG2b VH region [mice, mRNA Recombinant Partial, 355 nt].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-AUG-1995) M. Geiser, K-681.5.46, CH-4002, Basel, SWITZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geiser, M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Vertebrata; Eutheria; Rodentia; Sciurognathi; J
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larity 89.1%;
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/strain="Balb/C"
/db_xref="taxon:10090"
/dev_stage="12 weeks old"
/tissue_type="spleen"
/cell_type="lymphocytes"
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/product="antibody heavy chain variable region"
/db_xref="pID:e364666"
/db_xref="pID:g1518295"
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L/KTANGLINPNNGDTFYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCANDGYH
WYFDVWGAGTPVTVSS"
89 c 93 g 80 t
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Pred. No. 3.24e-186; 
0; Mismatches 36; Indels
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                                                                      GAGCTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTACAAGGAATGACCCC
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Mount,P.F., Sutton,V.R., Li,W., Burgess,J., McKEnzie,I.F.,
Pietersz,G.A. and Trapani,J.A.
Chimeric (mouse/human) anti-colon cancer antibody c30.6 inhibits
the growth of human colorectal cancer xenografts in scid/scid mice
Cancer Res. 54 (23), 6160-6166 (1994)
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Location/Qualifiers
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llarity 87.3%;
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/COGON_STATE-1
/POODICT="IG92b VH region"
/product="IG92b VH region"
/db_xref="pID:9688163"
/translation="QVCLQESCPELVKPGASVKISCKASGYTFTDYNNHWVKQSHGKS
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/translation="QVCLQESCPELVKPGASVKISCKASGYTFTDYNNHWVKQSHGKS
LEWIGFTYPYNAGTGYNQKFKNKATLTVDSSSSTAYMELRSLTSEDSAVYYCTRNDPH
WYFVVMGQGTTVTVSS"
80 t
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/gene="IgG V<down>H</down>
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Eutheria; Rodentia; Sciurognathi; I
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0; Mismatches 44;
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Best Local Similarity 89.1%;
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                                                                                                                                                                                                                                                                                                   CGAGACTATTCTATGGACTACTGGGGTCAAGGAACCTCAGCTCACCGTCTC 353
                                                                                                                                                                                                                                                                                                                                                            GAGCTCCTCAGTCTGACATCTGCGGACTCTGCAGTCTATTACTGTACAAGACGGGGGTTT 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACAGAACCTIGAGTGGATIGGACTIATTAATCCTTACAATGGTGGTACTAGCTACCAAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCAAGGCTTCTGTTTACTCATTCACTGGCTACACCATGAACTGGGTGAAGCAGAGCCAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGAAGCCTGGAGGTTCAATGAAGATATCC 424
                                                                                                                                                                                                                                                                                    CG-GACTGGTACTTCGATGTCTGGGGGGGCGCAGGGACCACGGTCACCGTCTC
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                                                                                                                                                                                                                                                                                                                                           GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG--GAGGGTTA
                                                                                                                                                                                 Sequence
178572
g3014726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 357)
Simpson,J.A., Chow,J.C., Baker,J., Avdalovic,N.M., Co,M.S., Vasquez,M., Britt,W.J. and Coelingh,K.L. Untitled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M95944
g309176
                                                                Queen,C.L., Schneider,W.P. and Selick,H.E. Polynucleotides encoding improved humanized Patent: US 5693761-A 84 02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (strain BALB/c, sub_species domesticus) cDNA Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; N
                                                                                                                           Unclassified
                                                                                                                                                         Unknown
                                                                                                                                                                                                                            178572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1992)
                                                                                                            (bases 1 to 414)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="domesticus"
/db_xref="taxon:10000"
/cell_line="MAb 5"
/cell_type="hybridoma"
1. .357
             a
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         /organism="unknown"
102 c 103 g
                                                      Location/Qualifiers
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87 c 88
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/strain="BALB/c"
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Pred. No. 1.00e-183;
0; Mismatches 35;
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Best Local Similarity 89.1%;
Matches 312; Conservative
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                                                        Matches
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GAGCTCCTCAGTCTGACATCTGCGGACTCTGCAGTCTATTACTGTACAAGACGGGGGTTT
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                                    CAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
178627
                                                                                                                                                                                                                                                      312;
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Humanized immunoglobulins
Patent: US 5693762-A 84 02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
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Similarity 89.18;
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Pred. No. 1.00e-183;
0; Mismatches 35:
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Pred. No. 1.00e-183;
0; Mismatches 35;
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605

GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG--GAGGGTTA

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SOURCE
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AUTHORS
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Best Local Similarity
Matches 312; Conser
 JOURNAL
                                   TITLE
                                                          AUTHORS
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                  1 (bases 1 to 421)
Takahashi, S., Matsuura, Y., Taniquchi, T., Tamura, H
Onishi, S., Yamamoto, Y., Yamamoto, H. and Fujimoto,
Molecular analysis of immunoglobblin heavy chain
idiotypic and anti-idiotypic antibodies involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 414)
Oueen, C.L. and Selick, H.E.
Humanized immunoglobulins
Patent: US 5585089-A 84 17-DEC-1996;
Location/Qualifiers
                                                                                                       Mus sp.
Eukaryotae;
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I31960
 Microbiol.
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            interaction
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102 c 103 g
Immunol.
                                                                                        mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Rodentia; Sciurognathi; Muridae; M
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Pred. No. 1.00e-183;
0; Mismatches 35;
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855-863 (1992)
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           Direct Submission
Submitted (24-NOV-1997) LMB, N
4B20, Bethesda, MD 20892-4255,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310;
                                                 2 (bases 1 to Chowdhury, P.S.
                                                                                         Rodentia; Sciurognathi;
1 (bases 1 to 723)
Chowdhury, P.S.
SS SCFV
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AF035617
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entry [NCBI gibbsq 121470] from the original journal article.
This sequence comes from Fig. 1.
Location/Qualifiers
                                                                                                                                              Eukaryotae; Metazoa;
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Similarity 89.3%;
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GYTFTDYYMKWVQSHGKSLEWIGDIRNNGGTSYNQKEKGKATLTVDKSSSTAYMQL
NSLTSEDSAVYYCARDYDDWTFDVWGAGTTVTVSSESQS"
a 100 c 113 g 102 t
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segment are shown completely;
partially"
Location/Qualifiers
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/db_xref="taxon:10095"
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Pred. No. 6.75e-183;
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                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 366)

E 6 Haard, J.J.W., Kazemier, B., Koolen, M.J.M., Nijholt, L.J.,

Meloen, R.H., van Gemen, B., Hoogenboom, H.R.M. and Arends, J.W.

Selection of recombinant, library derived antibody fragments

against p24 for application in HIV-1 diagnostics

Ciin. Diagn. Lab. Immunol. (1998) In press

E 2 (bases 1 to 366)

E 3 (bases 1 to 366)

E 4 Haard, J.J.W., Kazemier, B., Koolen, M.J.M., Nijholt, L.J.,

Meloen, R.H., van Gemen, B., Hoogenboom, H.R.M. and Arends, J.W.

Direct Submitted (01-AUG-1998) Functional Biomolecules, Unilever Research

Laboratorium Vlaardingen, Olivier van Noortlaan 120, Vlaardingen
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/db_xref="plD:g92139"
/db_xref="plD:g9
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/tissue_type="spleen"
/clone_lib="phage display library made from spleen mRNA
mice immunized with DNA"
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/strain="Balb/c"
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Mismatches 36;
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Rueff-Juy, D., Marche, P.N., Drapier, A.-M. and Cazenave, P.-A.
Junctional diversity of H and L chains allows the coexpression
two mutually exclusive idiotopes (IdI104 and IdI558)
                                                                                                                                                                                                                                                                                                                                                                         g193744
J-region; V-region; immunoglobulin
Mus musculus cDNA to mRNA.
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Vertebrata; Eutheria;
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/db_xref="piD:g3493269e"
/translation="QVQLQQSGPELVKPGASVKLSCKLSGYSFTGYTMNWVKQSHGKN
/translation="QVQLQQSGKFKGKATLIVDKSSSTAYMELLSLTSEDSAVYYCARDPYY
YGSSWYFDVWGAGTPVTVSS"
a 91 c 95 g 89 t
            /translation="MELDLSLPLVRNCRCLSEVOLOQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSPGKSLEWIGDISPNNGGTSYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGTGTTVTVSS"
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/product="Ab 16.3 heavy chain variable
regions"
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/strain="BALB/c"
/db_xref="taxon:10090"
/note="imm...i-
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/db_xref="taxon:10090"
/cell_line="hybridoma"
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Eutheria; Rodentia; Sciurognathi; N
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                                  273 CAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 332
                                                                                                                                             391 -ACTGGTACTTCGATGTCTGGGGCACAGGGACCACGGTCACCGTCTC 436
665 GACTGGTACTTCGATGTCTGGGGGGGGGGGACCACGGTCACCGTCTC 711
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Search completed: Sat Jan 9 15:24:33 1999 Job time: 540 secs.

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Perfect Score:
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Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result being and is derived by analysis of the total score distribution
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Copyright (c) 1993-1998 University of Edinburgh,
Distribution rights by Oxford Molecular L
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SUMMARIES

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711 711 711 462 462 462 417 10704 110844 11529 12132 443

T165006 T117728 Q5517728 Q5517728 T34542 T31541 T199435 T243843 Q43843 Q43844 Q43844 Q43844 Q43844 Q43844

Single-chain anti-erb
Anti-erbBZ ScFv cDNA.
Sequence encoding the
Monoclonal anti-idiot
3H1 heavy chain varia

4.40e-225 3.29e-222 3.26e-125 1.26e-165 1.26e-165 1.26e-160 6.39e-160 6.39e-160 6.39e-160 6.39e-160 6.39e-160 6.39e-160 3.21e-154

Anti-idiotype antibod Chimeric 128.1 VH, mo Plasmid pAH4625. Plasmid pAH4602. Plasmid pAH4602. Plasmid pAH4607. KM-750 heavy chain.

Hypercalcaemia agent

18 18 22 22 21 7 7 7

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erbB-2 protein, gp185 ction and treatment of ish.  a claimed single-chain p1B-2. Monoclonal antil h N/erbB-2 cells overebells and producing hybra coding for the antie converted to cDNA. Regin variable regions were encoding a peptintibody is useful for intibody is useful for intibody is useful for intibody is useful for intibody is useful for intibody.	(Fv) cDNA. on; light chain; heavy ch small cell lung carcinoma; c agent; erbB-2; ds.	Single chain anti-dis 3 Single chain anti-dis 3 Bispecific CD3-L6FVIg 8 Mouse anti-HIV mu5.5 Anti HIV antibody hea 2.1 Fv(GP-4) immunosuppre 1 Fv(GP-4) immunosuppre 2 Anti-DNA antibody 8d8 Anti-DNA antibody 8d8 Anti-DNA antibody 7d3 3 U7.6 heavy chain vari 3 ScFv U7.6 vH gene. 3 ScFv U7.6 vH gene. 3 Sequence encoding mou 3 Sequence encoding seque 1 A77 anti-Fc alpha R a 5 FB5 antibody heavy chain variable DNA encoding the heav 1 A0A encoding the heav 1 DNA e
- with tumour antibody, antibody e23 pody e23 professing idomas ribb-2 re then de n vitro	hain;	3.10e-149 3.10e-149 2.95e-144 2.95e-144 2.95e-141 1.06e-141 1.06e-141 1.06e-137 3.76e-137 3.76e-137 3.76e-137 3.76e-137 3.76e-137 3.76e-137 3.76e-133 3.76e-134 3.76e-133 3.76e-134 3.76e-

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RESULT ACCORDED TO THE PROPERTY OF THE PROPERT
                                                                                                                                                   Proposition of proliferation or survival of, esp. malignant erbB2, procells - by introducing nucleic acid mol. encoding antibody homologue procells - by introducing nucleic acid mol. encoding antibody homologue procells - by introducing nucleic acid mol. encoding antibody homologue procells - by introducing nucleic acid moles are sequence erbB2, protein intracellularly processed and binds, pref. erbB2, protein intracellularly processed and sequence encoding a signal peptide CC (R94019) linked to a second sequence (T17728) encoding a single CC (R94019) linked to a second sequence (T17728) encoding a single CC (R94019) linked to a second sequence (T17728) encoding a single CC (R94019) linked to a second sequence (T17728) encoding a single CC (R94019) linked to a second sequence (T17728) encoding a single CC (R94019) linked to a second sequence (T17728) encoding a single CC plasmid as template. The signal peptide directs the scFv to the CC plasmid or viral vector to facilitate expression of the scFv antibody composition of the homologue inhibits surface expression of erbB2 and CC thereby inhibits cell proliferation and cell survival and decreases
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23-AUG-1995; U10740.
06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
(UABR-) UAB RES FOUND.
Curiel DT, Deshane J;
WPI; 96-171307/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy;
Synthetic.
WO9607321-A1.
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T17728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncoprotein; erbB2; cell proliferation; tumour; cancer; intracellular antibody homologue; single chain antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis of tumour cells which overexpress the erbB-2 gp185 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours. Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;
                                                                                                                  tumorigenicity.
Sequence 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-erbB2
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Score 348; DB 29;
Pred. No. 4.40e-225;
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Best Local S
Matches 34
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WPI; 94-025878/03.
P-PSDB; R45442.
Treatment of malignancies over-expressing ERB-[2 - using at 7 monoclonal antibodies which recognise different epitopes (7 monoclonal antibodies which recognise different epitopes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoding the single chain Single chain anti-erbB1 antibody; c monoclonal antibody; ss.

Synthetic.

Kev
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The source of human erbb-2 protein for the prodn. of antibodies not provided the source of human erbb-2 protein for the prodn. of antibodies not provided to express the human erbb-2 protein on its surface (N/erbb-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbb-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;
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Q55180;
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30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY
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06-JAN-1994.
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346; Conservative
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28-DEC-1995; U17105.
28-DEC-1994; US-365484.
28-DEC-1994; US-365484.
(KENT ) UNIV KENTUCKY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to carcinoembryonic antigen
Example 2; Fig 2A; 102pp; English.
A cDNA clone (T34542) codes for the heavy chain variable region
(R99687) of monoclonal anti-idiotype antibody 3H1 (ATCC HB 12003
It was obtd. by PCR amplification (see also T34543-44) of cDNA
derived from 3H1 hybridoma cells. Anti-idiotype antibody 3H1
elicits a specific immune response to a unique epitope of
carcinoembryonic antigen (CEA) that is not present on other
members of the CEA family or on normal adult tissues. 3H1
can be used as a vaccine to elicit immune responses in pattents
with advanced CEA-associated disease or, when labeled, to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 4
T34542
T34542;
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106 A;
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Key
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Anti-idiotype antibody; monoclonal antibody; CEA;
carcinoembryonic antigen; tumour-associated antigen;
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90.0%;
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Pred. No. 1.26e-165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PT Recombinant monoclonal anti-idiotype antibody 3H1 sequences - used to develop prods. for the detection and treatment of carcinoembryonic antigen-associated diseases, partic. cancers PT Calaim 6; Fig 2A; 121pp; English.

CA CDNA clone (T31541) codes for the heavy chain variable region (CVH) (R98411) of 3H1, a murine monoclonal anti-idiotype antibody (CVH) (R98411) of 3H1, a murine monoclonal anti-idiotype antibody (CVH) (R98411) of 3H1, a murine monoclonal anti-idiotype antibody (CVH) (R98411) of 3H1, a murine monoclonal anti-idiotype antibody (CVH) (R98411) of 3H1, a murine monoclonal anti-idiotype antibody (CVH) (R98411) of 3H1, a murine monoclonal anti-idiotype antibody (CVH) (R98411) of carcinoembryonic antigen (CEA) and which elicits an immune response in patients with advanced CEA-associated disease, e.g. colorectal cancer. It was obtd. by PCR amplification of 3H1 hybridoma DNA (See also T31545-46). The isolated polynucleotide, and/or a polynucleotide (see also T31540) coding for the VL region (R98410) of 3H1 can be used to design probes and primers, in expression Systems, and in pharmaceutical applns, including vaccines, gene therapy and genetic immunisation, partic. against cancer.
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Anti-idiotype; monoclonal antibody; MAb; 3H1; C
carcinoembryonic antigen; cancer; gene therapy;
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04-JUL-1996.
28-DEC-1995; U17103.
28-DEC-1994; US-365484.
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WPI; 96-321850/32.
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                                                                                                    GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTG-CA--AGGAGGGTT
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Similarity 90.0%;
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Pred. No. 1.:
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PS Disclosure; Page 39; 66pp; English.

CThis cDNA sequence includes a coding region for the heavy chain variable region (VH) (see W26729) of murine monoclonal anti-idiotype antibody 3H1. A cDNA sequence (see T99434) for the VL region (see W26728) is also provided. These clones can be utilised in the recombinant production of 3H1 polypeptides. 3H1 induces a specific immune response against a distinct and specific epitope of carcinoembryonic antigen (CEA), a tumour-associated antigen. The invention provides methods of delaying development of CEA-associated invention provides methods of delaying development of tumours, including colorectal, gastric and pancreatic tumours, as well as other adenocarcinomas such as those of the breast and lung, and collising cancers.
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Best Local S
Matches 31
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23-OCT-1997; U05953.
11-APR-1997; US-631085.
12-APR-1996; US-631085.
(KENT) UNIV KENTUCKY.
Chatterjee M, Chatterjee Si
WPI; 97-256218/48.
P-PSDB; W26729.
    Chimeric 128.1 VH, mover Polymeran
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Q43843;
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T99435;
27-Apr.1998 (first entry)
Anti-idiotype antibody 3H1 heavy chain variable region Anti-idiotype antibody 3H1; carcinoembryonic antigen; tumour-specific antigen; tumour; colorectal cancer; luadenocarcinoma; therapy; ss.
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                                                     standard;
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315; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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 reaction; primer;
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90.08;
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  subgroup
mer; PCR;
amplify; murine;
             IIB DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; lung cancer;
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Best Local Similarity
Matches 302; Conser
A3846; d43846; d43846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Table 6; Page 57; 151pp; English.

Table 6; Page 57; 151pp; English.

The sequences given in Q43842-43 encode the light and heavy chains, respectively, of the chimeric antibody 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothellal cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods.

Sequence 417 BP; 108 A; 104 C; 102 G; 103 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUN-1993.
24-NOV-1992;
26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R38259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09310819-A
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US-800458.
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58..417
/*tag- b
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Pred. No. 6.39e-160;
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endothelial cell; conjugate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 417;
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Control Sequences given in Q43846-48 represent the expression vectors paH4625, paH4807 and paH4808. These vectors represent the cloning of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4 crespectively, with the variable region of the murine monoclonal contibody 128.1. These plasmids each encode a chimeric monoclonal contibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CHI, CH2 and CH3 are derived from a control 
                                                                                                                                                                                                                                                                                                             Matches
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                       2088
                                                                                                                                                                                    1968
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26-NOV-1991; US-800458.
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Key
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                                                                                                                                                                                                                                                                                                                              Local
cagaagttcaaggacaaggcccctttaactgtagacaagtcatccaacacagcctacatg
                                                                                99agagaaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac
                                                                                                                                                               tgcaaggcttctggttactcattcactggctacaccatgaactgggtgaagcagagccat 2027
                                                                                                                                                                                                                          GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGAAGCCTGGAGGTTCAATGAAGATATCC 424
                                                           TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
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                                                                                                                                                                                                                                                                                                             302;
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                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  and Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                            10704 BP;
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Sequence not given
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/note= "Undefined ORF2"
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/note= "Sequence
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/note= "Undefined ORF1"
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/note= "Chimeric
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                                                                                                                                                                                                                                                                                                                            73.9%;
                                                                                                                                                                                                                                                                                                                                                                                        2125 A;
                                                                                                                                                                                                                                                                                                                            Score 257; DB 7; I
Pred. No. 6.39e-160;
                                                                                                                                                                                                                                                                                                           0,
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The sequences given in 04386.48 represent the expression vectors cpAH4625, pAH4807 and pAH4808. These vectors represent the cloning cof the different human gamma isotypes, gamma-2, gamma-3 and gamma-4 respectively, with the variable region of the murine monoclonal antibody 128.1. These plasmids each encode a chimeric monoclonal cantibody in which the heavy chain (VH) is derived from a murine course and the sequences encoding CH1, CH2 and CH3 are derived from a human source. These vectors in combination with the chimeric light chain vector, pAG4611 (see also Q43845), were transfected into SP2/0 cells and clones were isolated. Antibody analysis using biosynthetically labelled proteins, immunoprecipitation and SDS-PAGE indicated appropriate bands for the heavy and light chains as well as the casembled antibody for the gamma-3 and gamma-4 chimeras. No detectable protein was isolated for the gamma-2 transfectants. 128.1 is an anti-
cused in a conjugate in which it is linked to a neuropharmaceutical or capinostic agent. The conjugate may be used to treat or prevent current control of the conjugate may be used to treat or prevent control of the conjugate may be used to treat or prevent control of the conjugate may be used to treat or prevent control of the conjugate may be used to treat or prevent control of the conjugate may be used to treat or prevent control of the conjugate may be used to treat or prevent control of the conjugate may be used to treat or prevent control of the conjugate may be used to treat or prevent control of the conjugate may be used to treat or prevent control of the control of the conjugate may be used to treat or prevent control of the co
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Q43848;
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P-PSDB; R41715-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-NOV-1991; US-8 (ALKE-) ALKERMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tactattctttggactactggggtcaaggaacctcagtcaccgtctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTGGTACTTCGATGTCTGGGGGCGCAGGGACCACGGTCACCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGAGGGTTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PM;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 19A-F; 151pp;
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; US-800458.
ERMES INC.
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6336..6635
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/note= "Undefined ORF3"
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/note= "Undefined ORF2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "Murine 128.1 VH/human gamma-4 CH1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note- "Undefined ORF1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..4611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stroke; epilepsy; monoclonal;
isease; SP2/0 cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-human; pAH4807;
                                                                                                                                      No detectable
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Best Local
                                                                                                                                                                                                                                                                                                                                                Q43844 standard; 1
Q43844;
20-OCT-1993 (fir:
Plasmid pAH4602.
WO9310819-A.
10-JUN-1993.
24-NOV-1992;
                                                                                                                                                                                                                                                                                  Plasmid pAH4602.

Polymerase chain reaction; primer; PCR; amplify; mu heavy; light; chain; variable; constant; region; ant transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methods.
Sequence
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                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                      665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9tccagctgcaacagtctggacctgaactggtgaagcctggagcttcaatgaagatttcc 4026
                                                                                                                                                                                                                                                                                                                                                                                                                    GACTGGTACTTCGATGTCTGGGGGCGCAGGGACCACGGTCACCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                               tactattctttggactactggggtcaaggaacctcagtcaccgtctc 4313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cagaagttcaaggacaaggcccctttaactgtagacaagtcatccaacacaccagcctacatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tycaagycttctgyttactcattcactgyctacaccatyaactgygtyaagcagayccat 4086
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Similarity 87.0%;
302; Conservative
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U10206
                          /*tag= n
8177..8201
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/note= "Leader
3964..4611
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/note= "VH
3097 .3963
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3907..4611
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/note= "Undefined
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/note= "Undefined
5163..5492
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/note= "Undefined
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/note= "Mature
                                                                                                                                                                                                                                                                   Location/Qualifiers
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Pred. No. 6.39e-160;
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                                                                                                                                                          VH/CH region'
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                                                                                                                                                                                                                   derived
                                                                                                                                                                                                                                                                                                                                      amplify; murine;
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                                                                                                                                                                                                                                                                                                                             region; anti-human;
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Disclosure; Fig 11A-G; 151pp; English.

This sequence represents the expression vector pAH4602.

This vector contains open reading frames encoding the heavy chain variable region (VH) of the antibody 128.1, an empicillin resistance gene and a histidine (histidinol) selection marker. Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin enhancer and the human gammal constant region (CH). The VH region of 128.1 was isolated by polymerase chain reaction and cloned into plasmid pAH4274. This was achieved by digesting the plasmid and the product with EcoRV and NheI. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The Conjugate may be used to treat or prevent neurological disorders and Alzheimers disease. It may also he used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 30
                                                                                                          Q43847 standard;
Q43847;
Q40-OCT-1993 (fir
Plasmid pAH4807.
           Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807 transferrin; recept; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epllepsy; monoclonal; disease; Alzheimers disease; SP2/0 cell; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic
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                                                                                                                                                                                                                             GACTGGTACTTCGATGTCTGGGGGCGCAGGGACCACGGTCACCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tactattctttggactactggggtcaaggaacctcagtcaccgtctc 4313
                                                                                                                                                                                                                                                                                                                                                                          GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGAGGGTTACG
                                                                                                                                                                                                                                                                                                          gagotcotcagtctgacatctgaggactctgcagtctattactgtgcaagaggctactat 4266
                                                                                                                                                                                                                                                                                                                                                         CAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                         ggagagaaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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11529 BP
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.98;
87.08;
                                                                                                                                                              12132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 257; DB 7; I
Pred. No. 6.39e-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of cancer, AIDS a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2217 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   It may also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurological
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The sequences given in Q43846-48 represent the expression vectors pAH4625, pAH4807 and pAH4808. These vectors represent the cloning of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4 respectively, with the variable region of the murine monoclonal antibody 128.1. These plasmids each encode a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1, CH2 and CH3 are derived from a human source. These vectors in combination with the chimeric light
                                                                                                                                                                                                                                                    chain vector, pAG4611 (see also Q43845), were transfected into SP2/0 cells and clones were isolated. Antibody analysis using biosynthetically labelled proteins, immunoprecipitation and SDS-PAGE indicated appropriate bands for the heavy and light chains as well as the assembled antibody for the gamma-3 and gamma-4 chimeras. No detectable protein was isolated for the gamma-2 transfectants. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-1993.
24-NOV-1992;
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; R41710-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALKE-) ALKERMES INC
                                               425
                                                                                                           365
                                                                                                                                                                                y Match 73.9%;
Local Similarity 87.0%;
                                                                                                                       gtccagctgcaacagtctggacctgaactggtgaagcctggagcttcaatgaagatttcc 1967
ggagagaaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac 2087
                                             TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT
                                                             tgcaaggcttctggttactcattcactggctacaccatgaactgggtgaagcagagccat 2027
                                                                                                       GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCC
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                                                                                                                                                                                                                               12132
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; US-800458.
                                                                                                                                                                  Conservative
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5566..5864
/*tag= h
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1848..2546
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6720..6744
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/note= "128.1 VH/human
/939..2980
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/note= "Undefined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Undefined ORF4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Undefined
3133..3177
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                                                                                                                                                                                                                              2292 A;
                                                                                                                                                                                 Score 257; DB 7; I
Pred. No. 6.39e-160;
                                                                                                                                                                   0;
                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                              2441 C;
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                                                                                                                                                                                                                              2285 G;
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KM-750 heavy chain.

Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody; expression vector; heavy; light; hypervariable region; CDR; constant region; hybridom hypervariable region; KM-796; KM-750; KM-603; cancer;
                                                                                   the Ab heavy and light chain variable region-encoding CDNA isolated from hybridomas producing a mouse or rat monoclonal Ab reacting with the ganglioside GM2 respectively into an expression vector for use in animal cells which contains the human Ab heavy and light chain constant region-encoding cDNA. The expression vectors are introduced into animal cells and the transformant thus obtained is cultured for the prodn. of a chimeric human Ab reacting with the ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric human Abs will not cause anti-mouse Ig Ab prodn. in the patient's body but show a prolonged blood half-life, with a reduced frequency of adverse effects, so that it can be expected to be superior to mouse monoclonal Abs in the efficacy in the treatment of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q45428;
17-NOV-1994
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                                    Cancer, for instance.

Cancer, for instance.

Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603

Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603
                                                                                                                                                                                                                                                                                                            Humanised antibody specific for ganglioside GM2 producing a cytocidal effect on cancers such as
                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1992; JP-238452
(KYOW ) KYOWA HAKKO KO
                        heavy and light chain sequences are CDR regions for use in chimeric Abs
                                                                                                                                                                                                                                                                                                                                                                        Shitara K;
                                                                                                                                                                                                                                                                                                                                                                                       Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                               AU9346181-A.
17-MAR-1994.
                Features Table.
                                                                                                                                                                                                                                                                    Chimeric human Ab expression vectors are constructed by inserting
                                                                                                                                                                                                                                                                               neuroblastoma and glioma.
Disclosure; Page 107-108; 191pp;
                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1993;
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33..89
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/note= "hypervariable
252.287
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180..194
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are indicated
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                                                                                                                                                                                                                                                                                                 Disclosure; Page 14; 18pp; Japanese.

The sequences given in Q28522-23 encode fragments which were used in the construction of an agent for the treating and prevention of hypercalcaemia. The agent contained a portion of the antihuman parathyroid hormone-related protein monoclonal antibody (antihuman PTHrP MAb). The MAb was used as the active component in the agent. The agent further comprises a rodent/human chimeric MAb which has a rodent variable region and a human constant region and recognises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment and preventive agent for hypercalcaemia - contg. one anti-human para-thyroid-hormone-related protein monoclonal antia a rodent or chimera monoclonal antibody, fused gene and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypercalcaemia agent cDNA portion 1.

Antihuman parathyroid hormone-related protein; monoclonal antibody; variable region; rodent/human chimeric MAb; constant region; PTHrP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q28522 standard;
Q28522;
23-FEB-1993 (fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-1991; 110565.
15-MAY-1990; JP-124581.
(KANF ) KANEKA CORP.
WPI; 92-320987/39.
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                            human PTHrP
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tgcaaggcttctggttactcatttactggctactttatgaactgggtgatgcagagccat
                                                                                              gttcagctgcagtctggacctgagctggtgaagcctggggcttcagtgaagatatcc
                                                                     GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGAAGCCTGGAGGTTCAATGAAGATATCC
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85.9%;
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d. No. 2.27e-151;
Mismatches 48;
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. No. 3.21e-154;
Mismatches 49;
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                                                                                                                                                                                                                                                                 103 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ry useful to detect tumour cells expressing GD2 and to target

ry therapeutic agents, e.g. toxins, to such cells

Disclosure; Page 11; 31pp; English.

CC The present sequence encodes a recombinant single chain peptide,

CC STI1-scFv. The peptide is an antibody construct comprising the variable

CC cregions of the heavy and light chains of an antibody against

CC distaloganglisside (GD2) as a single chain Fv fragment (scFv). GD2 occurs

CC in many tumours types including neuroblastoma, osteosarcomas and other

CC soft tissue sarcomas, medulloblastomas, high grade astrocytomas,

CC melanomas and small cell lung cancer. The peptide can be detectably

CC distaloganglisside (GD2) as a toxin, streptide can be detectably

CC distaloganglisside cell lung cancer. The peptide can be detectably

CC distaloganglisside cell lung cancer. The peptide can be detectably

CC melanomas and small cell lung cancer. The peptide can be detectably

CC distaloganglisside cell lung cancer. The peptide can be detectably

CC melanomas and small cell lung cancer. The peptide may further

CC converting enzyme, to cells expressing GD2. The peptide may further

CC comprise CD8 to facilitate the formation of GD2-targeted lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour cells.
717 BP;
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Single chain anti-disialoganglioside GD2 antibody 5F11-scFv.
Antibody construct; disialoganglioside; GD2; single chain Fv fr.
scFv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma;
tissue imaging; target delivery; toxin; streptavidin;
tissue imaging; converting enzyme; GD2-targeted lymphocyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant single chain anti-disialoganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheung NV, Guo H, Larson WPI; 97-479996/44.
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20-MAR-1996; US-013703.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SLOK ) SLOAN KETTERING INST CANCER Cheung NV, Guo H, Larson SM, Rivlin
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cagaagttcaagggcaaggccacattgactgtagacaagtcctccagcacagcctacatg
                                                                                          TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT
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86.7%;
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Pred. No. 3.10e-149;
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76 21.8 431 11 AA710970 vt93h09.r1 Soarcs mous 3. 71 20.4 287 16 T27609 EST101034 Homo sapiens 7. 8 19.5 336 15 AA987559 or83g01.s1 NCL_CGAP_Lu 1. 66 19.0 25 AA377128 EST8960 Small intesti 1. 66 19.0 291 25 AA377074 EST89603 Small intesti 64 18.4 488 15 AA948436 on67a01.s1 Soarcs_NFL_ 1.	5.60 46.0 310 18 AI180569 uc70f09.rl Soares mous 9.  4.6 42.0 294 15 AI007196 ua73g04.rl Soares ZNDM 1.  1.0 31.6 387 9 AA569186 nm30d10.sl NCI_CGAP_Li 1.  85 24.4 279 24 AA300571 EST13661 Testis tumor 5.  85 23.6 379 8 AA291381 zt44902.rl Soares ovar 1.  81 23.3 209 16 T28938 EST61186 Homo sapiens 7.  79 22.7 116 17 AI116736 uc18e08.rl Soares mous 7.	SUMMARIES Query Query Ce Match Length DB ID Description Pre	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being print and is derived by analysis of the total score distribution.	atabase: emb1-est55 1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 atabase: genbank-est107 5:gb_est1 6:gb_est107:gb_est11 8:gb_est129:g) 10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est11 14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20 18:gb_est21 19:gb_est3 20:gb_est4 21:gb_est20 23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27 28:gb_gss3 29:gb_gss4	Post-processing: Minimum Match 0% Listing first 45 summaries	Nmatch STD : Dbase 0; Query 0 Searched: 2275026 seqs, 895388244 bases x 2	Title: >US-08-704-178-1 Description: (364-711) from US08704178.seq (3 of 4) Perfect Score: 348 N.A. Sequence: 364 TGTGCAGGTCAGGTCAGGTCACCGTCTC Comp: ACACGTCGACGTCCTCAGTCCCCTGGTGCCAGTGGCAGAG Scoring table: TABLE default Gap 6	MPsrch_nn n.a n.a. database search, using Smith-Waterman algorithm Run on:  Sat Jan 9 15:24:53 1999; MasPar time 491.43 Seconds 1268.112 Million cell update Tabular output not generated.	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	
1.19e 1.32e	1.51e- 1.76e- 5.47e- 1.37e- 2.06e-	1 H	ye av	gg dg			ACCGTCTC 711 TTGGCAGAG	orithm conds updates/sec	. 3	‡ <u> </u>

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.59e-2	.59e-2	.33e-2	.33e-2	.33e-2	.43e-2	.43e-2	.43e-2	.43e-2	.43e-2	.66e-2	.66e-2	.66e-2	.66e-2	.23e-3	.23e-3	.37e-3	.37e-3	.37e-3	.37e-3	.42e-3	.52e-4	.61e-4	.19e-5	.35e-5	.45e-6	.05e-6	.15e-6	.15e-6	.23e-6	1.35e-70	.39e-7	

# ALIGNMENTS

source	FRATURES					COMMENT	JOURNAL	ח דחד מ				AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION		DEFINITION	Locus	RESULT 1
1. 310 /organism="Mus musculus" /strain="C57BL/6J"	Seq prime: -28ml3 rev2 ET from Amersham.	This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information.	Fax: 314 286 1800 Fax: 314 286 1810 Fax: 314 286 1810	Washington University School of MedicineP	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project		Unpublished (1996)	Waterston, R.	Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and	Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,	Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,	1 (bases 1 to 310)	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	Mus musculus	house mouse.	EST.	g3731207	AI180569	(HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene	1431017 5' similar to ob:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION	AII80569 310 bp mRNA EST 08-OCT-1998	

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DEFINITION
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Contact: Marra M/Mouse EST Project washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lt Tel: 314 286 1800
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheri; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 294)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubles, M., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                              AI007196 294 bp mRNA EST 12-JUN-1998 ua73904.rl Soares 2NbMT Mus musculus cDNA clone 1363158 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                       The WashU-HHMI Mouse Unpublished (1996)
                                                                                                                                                                                                                                                                                                                               Mus musculus
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RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /notem Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Site_2: Eco RI; lst strand cDNA was primed with oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="mammary gland"
/dev_stage="4 weeks"
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/clone="1431017"
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77 c 85 g
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79.3%;
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Pred. No. 9.99e-288;
0; Mismatches 58;
                                                                                                                                          EST Project
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                   Louis,
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                                                                                                                                                                                                                                                                                                                         TCAAAAGTTCAAGGACAAGGCCACATTGACTGTAGACAAATTCACCAGCACAGCCTACAG
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                                                                                                       g2342240
EST.
                                                                                                                                                         AA569186 387 bp mRNA nm30d10.s1 NCI_CGAP_Lip2 Homo similar to gb:L02325 IG HEAVY
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 387)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy
                                                        Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata;
                                                                                        human.
                                                                                                                                   AA569186
                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor
Seq primer: -28m13 rev2 ET from
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:896378
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larity 76.7%;
Conservative
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="1363158"
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/strain="C57BL/6J"
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                                                                                                                                                           Sapiens cDNA clone
CHAIN PRECURSOR V-1
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                                                           Mammalia;
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IMAGE:1061683
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                                                                                                                                                                                                                                                                                                                                              338 GAGCTTAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCGAG
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Location/Qualifiers
1. .387
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Seq primer: -40ml3 fwd.
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                                   Eukaryotae; mitochondı
Vertebrata; Mammalia;
                                                                           Homo sapiens
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                                                                                                                                                                                                             EST13661 Testis
                                                                                                                                                                                                                                 AA300571
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Similarity 69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www-bio.llnl.gov/bbrp/image/image.html
                                                                                               numan.
(bases 1 to 279)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Organism="Homo sapiens"
/note="Vector: pANF10; mRNA made from liposarcoma, cDNA
made by oligo-dT priming. Non- directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robert Strausberg,
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/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
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                                   mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Pred. No. 1.76e-177;
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bedharik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
                                                                                                     G
                                                                                                                                                                                                                                                                               GGACAAGGGCTTNAGTGGATGGGATGGATCAACCCTAAAAGTGGTGGCACAAACTATGCA 271
                                                                                                                                                                                                                                                                                                                                                                               TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT
zt44g02.rl Soares ovary 5' similar to gb:M18512 (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser.C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence based upon 83 million nucleotides of cDNA sequence 377 (6547 Suppl), 3-174 (1995)
                                                                              AA291381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi/html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 3018699056
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EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):192212"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
<1. .>279
74 c 85 g
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Pred. No. 5.47e-124;
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                                                                                                                                                                                                                                              GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                              GAGCTGAGGAACCTGAGATCTGACGACACGGCCATATATTACTGTGCGAG 324
                                                                                        GGGAGTTTTCAGGACAGAGTCAGCTTGACCACTGACATCCACGAATACAGCCTACATG
                                                                                                                                                                                    TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT
                                                             CAGAAGTTCAAGGGCAAAGTTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG
                                                                                                                        ch 23.6%;
l Similarity 65.9%;
191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1576 Std Error: 0.00 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 379)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
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Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin
<1. _>379
82 c 121 g 91 t
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/clone="725234"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares ovary tumor NbHOT"
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0; Misma
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Best Local Similarity 71.7%;
Matches 134; Conservative
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                                                                                                         453
                                                                                                                                  135 CTAGTGAAGGTGTATCCAGAAGCCTTCCAGGAAACCTTCACTGAGGCCCCAGGCTTCTTC 194
                                                                                                                                                                                                                      513
                                                    195 ACCTCAG 201
                                                                                                                                                                                                                                                                                                                       573 GTAAATGTGGCCCTTGCCCCTTGAACTTCTGGTTGTAGTATCACCATTGTAAGGATTA 514
                                                                                                                                                                                                                                                                                                                                                      15 GTAATGGTGACTCTGCCCTGGAACTTCTGTAAATATTTTGTGTTACCATTGCCAGCGTTG 74
                                                                                                                                                                                                                                      75 ATCCATCCCATCCAAGCCTTTGTCCGGGGGCCTGGCGACCCAATGCATAGCATAG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Radams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarth, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrite, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kin, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Trittal Bescenart of Human Cone Divorsity and Fennession Datterns
                                                                                                      CCAGTGAATGAGTAACCAGAAGTCTTGCAGGATATCTTCATTGAACCTCCAGGCTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute fo. 932 Clopper Rd, ( Tel: 3018699056 Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T28938
g611036
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amiota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST61186 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Venter, JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tdbinfo@tdb.tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human primer-M13 Reverse library-Human White blood cells
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387
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<1. .>209
1 62 c 48 g 5
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81; DB 16; L
Pred. No. 1.37e-115;
0; Mismatches 53;
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                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                 546
    606 AGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                                                                                                                                                                       Local
                                                                                                                        2 AGAAGTTCAAGAACAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGC 61
                                                                             AACTCAGCAGCCTGACATCTGAGGACACTGCGGTCTATTACTGTGGAAG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uclee08.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone 1398374 5' similar to gb:x87789 IG GAMMA-1 CHAIN C REGION (HUMAN); gb:x87210 M.musculus rearranged immunoglobulin gamma 2b heavy (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 116)

Marra,M., Hillier,L., Allen,M., Le,M., Martin,J., Morris,M.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g3516560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trace considered overall poor quality Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae;
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94; Conse
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314 286 1810
                                                                                                                                                                 22.7%;
larity 86.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
32 c 25 g 21 t
                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="1398374"
/clone_lib="Soares mouse mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo
                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on/Qualifiers
                                                                                                                                                               Score 79; DB 17; L
Pred. No. 2.06e-111;
0; Mismatches 15;
                                                                                                                                                                                                        Length 116;
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KEYWORDS
SOURCE
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ORIGIN
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Best Local
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                                                                                                                                                                                                   124 AGTCTGGACCTGAAGAAGAAGCCTGGAGAGACAGTCAAGATCTCCTGCAAGGCTTCTG 183
                                                                                                                                                       378 AGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCCTGCAAGACTTCTG
                    244 AGTGGATGGGCTGGATAAACACCTACTCTGGAGTGCCAACATATGCTGATGACTTCAAGG 303
                                                                 GTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTG
                                                                                                           GGTATACCTTCACAACCTATGGAATGAGCTGGGTGAAACAGGCTCCAGGAAAGGGTTTAA 243
vt93h09.rl Soares mouse mammary gland NDMMG Mus musculus cDNA clone 1178753 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:X70423 M.musculus mRNA for monoclonal antibody heavy chain gamma (MOUSE);, mRNA sequence.

AA710970
g2720888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra, M., Hillier, I., Allen, M., Bowles, M., Dietrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, J.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project Unpublished (1996)
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1 (bases 1 to 431)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Econe RI sites of the modified pT773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                 /dev_stage- - ...
/lab_host="DH10B"
'103 c 112 g
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="1178753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares mouse mammary gland NbMMG'
                                                                                                                                                                                                                                                                  21.8%;
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                                                                                                                                                                                                                                                                  Score 76; DB 11; L
Pred. No. 3.58e-105;
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                                                                                                                                                                                                                                  Local
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Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J. Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of CDNA Sequence
                            TGCAAGACTTCTGGATACGCCTTCACCGACTACTATATACACTGGATTCGACAGGCCCCT 193
                                                                                                 GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCC 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tdbinfo@tdb.tigr.org

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression

For clone availability additional sequence the TIGR D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Resu
932 Clopper Rd, Gaithersburg,
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ost
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 287)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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larity 70.3%;
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                                                                                                                                                                                                Score 71; DB 16;
Pred. No. 7.44e-95;
0; Mismatches 52
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Matches 17
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365 GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCC 424
                                                                                                         92 TGCTTGGCCTCTGGAGGCACCTTCGGTAGTTCGACTGTCAGCTGGGTGCGACAGGCCCCT 151
                                                                                                                                                                                          32 GTCCAGATAGAACAGTCAGGGGCTGAGGTGAAGGCCAGGGTCTTCGGTGAAGGTCACC 91
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                                       GGACAACGGCCTGAGTGGATGGGGAAGATCATCCCCATCGCTCATTCAGCGAACTACGCA 211
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                                                                                   TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
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or83g01.s1
similar to
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179; Conser
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., P
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                    19.5%;
larity 61.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:1602480"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
a 86 c 100 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Organism="Homo sapiens"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
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gb:M87789 IG
                                                                                                                                                                                                                                                 Score 68; D. Pred. No. 1.00 0; Mismatc
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Homo sapiens cDNA clone IMAGE:1602480
GAMMA-1 CHAIN C REGION (HUMAN);, mRNA
                                                                                                                                                                                                                                                    No. 1.02e-88;
Mismatches 111; Indels
                                                                                                                                                                                                                                                                                             DB 15;
                                                                                                                                                                                                                                                                                           Length 336;
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             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Woreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Lii,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Zu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGAAGTTTCAGGACAGAATCACAATAACCGCGGACAAATCTACGGCGTCAGTCTACATG
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EST.
                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human
Index (http://www.tigr.org/tdb/hg1/hg1.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA377128 265 bp mRNA EST 21-APR-1997
EST89660 Small intestine I Homo sapiens cDNA 5' end similar to
similar to immunoglobulin heavy chain, VDJ region, mRNA sequence.
AA377128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_ESTs: THC167579
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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ms,M.D., Kerlavage,A.R., Fleischmann,R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute for Genomic Research
2 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                            57
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 (6547 Suppl),
                                                                                                                                                                                   /note="Organ: small intestine; '
Site_1: EcoRI; Site_2: xhoI"
   /db_xref="RTCC (inhost):181546"
   /db_xref="taxon:9606"
   /clone_lib="Small intestine I"
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                    /dev_stage="adult"
                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                       19.0%;
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69 c
                   Score 66; DB 25;
Pred. No. 1.19e-84;
0; Mismatches 49
                                                                                                                            79
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                                                                                                                                                                                                                                                                    intestine; Vector: pBluescript SK-;
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                                                                                                                            H
                                                           Length 265;
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                     Indels
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                   0;
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                   Gaps
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mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 37
96026280
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EST.
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AA377074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                               Fax: 3018699423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 8 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGGCTCGAGTGGATGGGATGATCACCGGTTACAATGGT 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                    Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone availability, addinformation related to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 291)
                                                                                                                               /note="Organ: small intestine; Site_1: ECORI; Site_2: XhOI"
/db_xref="APCC (inhost):181500"
/db_xref="taxon:9606"
                                                            /dev_stage="adult"
                                                                                                      /clone_lib="Small
                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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73 c
   89
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                                                                                                      intestine
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   1 others
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 CAGAAGTTTCGGGGGAGAGTCAC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 GTGCAGCTGGTGCAATCTGGGGCTGAGGTGAAGGAGCCTGGGTCTTCTGTGAAAGTNTCG 134
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18.4%;
1 Similarity 71.4%;
115; Conservati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA948436 488 bp mRNA EST 23-JUN-1998 on 07a01.sl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1561704 3' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 19.0%;
1 Similarity 66.0%;
134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 48)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g3109689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 naman
                                                                                                       108
                                                                                                                                                                                      /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-303087, 682632-687239, 726408-728711, and 72996-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene Index
                                                                                                                     /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                        /clone="IMAGE:1561704"
                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
   Score 64; DB 15;
Pred. No. 1.32e-80;
0; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 25; Length 291, Pred. No. 1.19e-84; 0; Mismatches 69; Indels
                                                                                                 88 g
     Mismatches 45;
                                                                                                   181 t
                                       DB 15; Length 488;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
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                                                                                                                                                               Query Match 17.8%;
Best Local Similarity 72.8%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                 source
163 TGCAAGGCTTCTGGTTACACCTTTACCAGCTACGGTATCAGCTGGGTGCGACAGGCCCCT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 GTATCACCATTGTAAGGATTAATAAGTCCAATCCACTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 GTGTTACCATTGCCAGCATTGATCCACCCA-TCCACTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 GTGCTCATGGACGTGTCCCTGGTTATGGTGACTCTGCCCTGGAACTTCTGTGCATATGTT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 CTCGCACAGTAATACACGGCCATGTCCTCAGATCTCAGGCTGCTCAGCTCCGTGTAGGCT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria; Archonta; Primates; Catarrini; Hominidae; Homes

1 (bases 1 to 238)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,

Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

FitzGerald, L.M., FitzHugh, W.M., Fritchmann, J.L., Geoghagen, N.S.M.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,

Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,

Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,

Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,

Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,

Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,

Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,

Fischer, C., Hastings, G.A., He, W., Hu, J.-S., Greene, J.M.,

Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunssch, C., Ji, H., Li, H.,

Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,

Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,

Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns

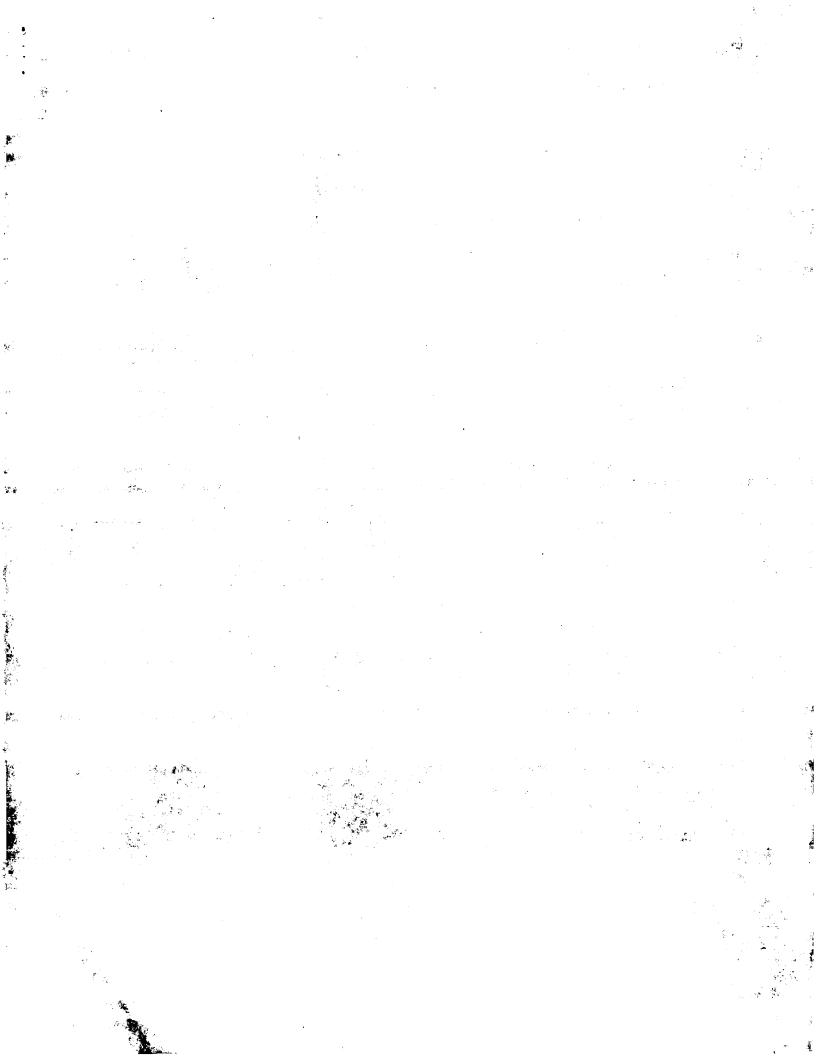
Based Upon 52 Million Basepairs of cDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
                                                     GTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGGCCTCAGTGAAGGTCTCC 162
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Rese
932 Clopper Rd, Gaithersburg,
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T29670 238 bp mRNA E9 EST89669 Homo sapiens cDNA 5' end similar chain V region (GB:X61012) (HT:3230).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Day (tdbinfo@tdb.tigr.org).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                  46
                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens" <1. .>238
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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70 c
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                                                                                                                                                            Score 62; DB 16; Le
Pred. No. 1.39e-76;
0; Mismatches 37;
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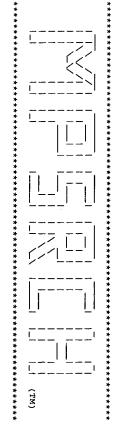
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TITLE
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ORGANISM
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                   691
201 R-SYTCVRKYCVMWMTKKV--VKKYHVVBBGCHBTDSKCKTMWMTNKHVMTSTTD 252
                                                                                 141
                                                                                                                      631 GTCCTCAGATGTCAGACTGAGGAGCTCCATGTAGGCTGTGCTGGACGACTTGTCTACAGT 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 GGACAAGGGCTTGAGT 238
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                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                             CWBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRAT 200
                                                                                                                                                          BVBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMW 140
                                          AAATGTGGCCTTGCCCTTGAACTTCTGGTTGTAGTTAGTATCACCATTGTAAGGATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. a
Suwon, Kyunggido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 252) Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.
Large-Scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g2801165
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA clone 97SN1787, mRNA sequence. AA754459
                                                                                                                                                                                                                                                                            h 17.0%;
Similarity 11.1%;
26; Conservative :
                                                                                                                                                                                                                                                                                                                                                                              G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4530"
/clone="97SN1787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/cultivar="Milyang23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                            Score 59; DB 12; Le
Pred. No. 1.35e-70;
120; Mismatches 86;
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                                                                                                                                                                                                                                                                                                                 Length 252;
                                                                                                                                                                                                                                                                              Indels
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511 AAGTCCAATCCACTCAAGGTTCTTTCCATGGCTCTGCTTCACCCAGTTCATGGTG 457

Search completed: Sat Jan 9 15:33:13 1999 Job time : 500 secs.





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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat Jan 9 17:10:52 1999; MasPar time 100.47 Seconds 921.250 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-08-704-178-1 (322-363) from US08704178.seq (4 of 4)

322 AGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG 363
TCCAAGATGGAGACCAAGACCATTTAGAAGACTTCCATTTCC

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries 567134 seqs, 1101898692 bases x 2

Database:

1:em\_ba 2:em\_fun 3:em\_htg 4:em\_hum1 5:em\_hum2 6:em\_in
7:em\_om 8:em\_or 9:em\_ov 10:em\_pat 11:em\_ph 12:em\_pl
13:em\_ro 14:em\_vi
genbank107

Database:

15:gb\_bal 16:gb\_ba2 17:gb\_htg 18:gb\_in 19:gb\_om 20:gb\_ov 21:gb\_pat 25:gb\_ph 23:gb\_pl 24:gb\_pl 25:gb\_pr1 26:gb\_pr2 27:gb\_pr3 28:gb\_ro 29:gb\_st 30:gb\_sts 31:gb\_sy 32:gb\_un 33:gb\_vi

Statistics: Mean 7.713; Variance 4.202; scale 1.836

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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11 12 13	8 9	765	4321	Result No.
20 20	24 24 24	34 30	42 38 34	Score
47.6 47.6 47.6	57.1 57.1 57.1	81.0 73.8 71.4	100.0 100.0 90.5 81.0	% Query Match
ь			711 711 720 846	Length
23 24	31 31	28 21 21	21 21 28	L DB
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8.14e+00 8.14e+00 8.14e+00	5.35e-02 5.35e-02 5.35e-02	5.00e-08 3.74e-06 1.54e-05	3.22e-13 3.22e-13 1.36e-10 5.00e-08	Pred. No.

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sapiens Xp22 sapiens Chro	ens Chromoso ens BAC clon		Arabidopsis thaliana B	S)	Arabidopsis thaliana q	sapiens	Homo sapiens gene for	S.pombe chromosome III	S.cerevisiae sequence	Arabidopsis thaliana g	hromosome I	ar sli	virus	Visna virus Icelandic	Visna lentivirus compl		Visna virus RNA genome		virus provi	Rattus norvegicus clon	visiae chro	Rattus norvegicus clon	rus cosmid-de	STS SHGC-189	Human DNA sequence fro	ŝ	Human papillomavirus t
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## ALIGNMENTS

DEFINITION Sequence 1 from patent US 5587458.  ACCESSION 132406 711 bp DNA DEFINITION Sequence 1 from patent US 5587458.  ACCESSION 132406 NID SOURCE UNknown.  ORGANISM Unknown.  ORGANISM Unknown.  ORGANISM Unclassified.  1 (bases 1 to 711) Atti-crbB-2 antibodies, combinations thereof, and therapeutic and diagnostic uses thereof JOURNAL Patent: US 5587458-A 1 24-DEC-1996; FEATURES Location/Qualifiers 1.0711 Coation/Qualifiers 1.0717 175 a 182 c 190 g 164 t ORIGIN  Query Match 100.0%; Score 42; DB 21; Length 711; Best Local Similarity 100.0%; Pred. No. 3.2e-13; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  DB 321 AGGTTCTACCTCTGGTTATGGTAAATCTTCTGAAGGTAAAGG 362					
ent US 5587458.  przyk, P.G. and Bird, R.E. ies, combinations thereof, A 1 24-DEC-1996; and lifers "unknown" 190 g 164 t 190 g 164 t 190 g 164 t 191 g 164 t TARATCTTCTGAAGGTAAAGG 362	z		Query Ma Best Loc Matches	SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURC BASE COUNT	RESULT LOCUS DEFINITION ACCESSION NID
	\$39590 711 bp anti-erbB2 immmunotoxin antigen binding \$Ynthetic Recombinant Partial, 711 nt]. \$39590 g251113 . Mus sp.		Score 42; DB 21; Pred. No. 3.22e-13; 0; Mismatches 0		711 bp DNA 1 from patent US 5587458.
07-JAN-1997  therapeutic and  0; Gaps 0;  0; Gaps 0;  10-FEB-1993 ice, Other	region [m.	362 363	ength 71:		. TAT
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91823198
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1 (bases 1 to 720)

King, C.Richter, Kasprzyk, P.G. and Bird, R.E. Anti-erbB-2 antibodies, combinations thereodiagnostic uses thereof patent: US 5587458 A 2 24-DEC-1996;
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Eukaryotae;
Vertebrata;
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42; Conservative
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larity 95.2%;
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182 c 190 g
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/db_xref="taxon:10095"
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Pred. No. 1.36e-10;
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Pred. No. 3.22e-13;
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antibody.
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Paul, S., Sun, M. and Gao, Q.-S.
Catalysis by natural and hybrid
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                  Similarity
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  Conservative
                                                                                                                                                       /note="c-myc peptide-1; putative"
/function="facilitates recombinant
775. 792
                                                                                            /note="poly-histidine; putative"
/function="facilitates recombinant
203 c 228 g 202 t
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LEWVATISGDTYTYYPDSVKGRFTISRDNAKNNLFLQMSSLRSEDTALYFCGRGIAY
                                                                                                                                                                                                                                                                                                                           /note="This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal."
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/product="antibody heavy chain"
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/product "antibody"
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/db_xref="PID:g896290"
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FGGGTKLEIKRADAAPGSTSGSGKSSEGKGGVKLVESGGGLVKPGGSLKLSCAASGFT
FSIYGMSWFFQTPEKKLEWTATISGDTYTYYPDSVKGRFTISRDNAKNNLFFQMSSL
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PGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQT
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Pred. No. 5.00e-08;
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354 AGGTTCTACCTCCGGCTCTGGGAAATCGTCTGAAGGTAAAGG

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antibody.
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L43544
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Similarity 90.5%;
38; Conservet'
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Paul.5., Sun,M. and Gao,Q.-S.
Catalysis by natural and hybrid single
Unpublished (1995)
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Vertebrata; Eutheria; Rodentia; Sciurognathi; J
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/db_xref="pID:9896294"
/db_xref="pID:9896294"
/translation="bythmyOrpelTLSVTIGOPASISCKSSQSLLHTDGKTYLIWLLQR
/translation="bythmYOrpelTLSVTIGOPASISCKSSQSLLHTDGKTYLIWLLQR
PGQSPKRLIYLVSKLDSGVPDRFTGSGSGSTDFTLKISRVEAEDLGVYYCWQGTHFPQT
PGQGTKLEIKRADAAPGSTSGSGKSSECKGQVQLQESGPGLVAFSQSLSITCTVSGFS
LTGYGVNWWRQPPGKGLEWLGMWGDONTDYNSALKSRLSISKDNSKSQVFLKMNSKI
LTGYGVNWWRQPFGKGLEWLGMWGDGTTVTVSSTKTTPPSVYPAAAHHHHHHGAAEQKLIS
                                                                                               /note="poly-histidine; putative"
/function="facilitates recombinant
217 c 217 g 190 t
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/translation="DVLMTQTPLTLSVTIGQPASISCKSSQSLLHTDGKTYLIWLLQR
PGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQT
FGGGTKLEIKRADAAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="This CDS feature is included to show the translation of the corresponding V_{\rm region}. Presently translation qualifiers on V_{\rm region} features are illegal."
                                                                                                                                                      /note="c-myc peptide-1; putative"
/function="facilitates recombinant
784 . .801
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                                                                                                                                                                                                                              /db_xref="PID:9896293"
/translation="OVQLQESGPGLVAPSQSLSITCTVSGFSLTGYGVNWVRQPPGKG
LEWLGMINGONTDYNSALKSRLSISKDNSKSQVFLKNNSLHTDDTARYYCARERDYR
LDYWGQGTTVTVSS"
                                                                                                                                                                                                                                                                                                                       translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal."
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/db_xref="taxon:10090"
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Score 34; DB 28;
Pred. No. 5.00e-08;
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g1823204
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King, C.Richter, Kasprzyk, P.G. and Bird, R.E.
Anti-erbB-2 antibodies, combinations thereo
diagnostic uses thereof
Patent: US 5587458-A 8 24-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I (bases 1 to 47)
King, C.Richter, Kasprzyk, P.G. and Bird, R.E.
Anti-erbB-2 antibodies, combinations thereodiagnostic uses thereof
Patent: US 5587458-A 9 24-DEC-1996;
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I32414
g310725
IgM-binding protein;
monoclonal antibody.
                                      SYNBET2X 717 bp mRNA
Synthetic single-chain Fv fusion protein (Bet 2/212) mRNA,
constructed from variable light and heavy chain regions of rat
monoclonal antibody Bet 2, 3 end of cds.
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7 c 16 g
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9 c 10 g
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patent US 5
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Pred. No.
0; Misma
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Pred. No. 3.74e-06;
0; Mismatches C
         fusion
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d. No. 1.54e-05;
Mismatches 0;
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9207839
7A41/212 SCA protein; fusion protein; monoclonal antibody; single-chain antigen-binding protein.
Mouse DNA and synthetic DNA.
artificial sequence
artificial sequence.
1 (bases 1 to 743)
1 (bases 1 to 743)
5. Lee,T.K., Posner, B.A., Filpula,D.R., Dodd,S.W., Finkelman,M.A.
Construction and characterization of a single-chain catalytic
                                                                                                                                                                                                                                                                                                                                                                             SYN7A41 743 bp DNA SYN 04-MAR-1993 Synthetic single-chain antigen-binding protein gene (7A4-1/212 SCA) constructed from the antigen-binding (Fab) fragment of mouse catalytic monoclonal antibody NPN43C9 and linker DNA, partial cds.
                                                                                                                                                                        antibody
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1 (bases 1 to 717)

Lee, T.K., Rollence, M.L., Hallberg, P.L., Oelkuct, M.S., Dodd, S.W.,
Nagle, J.W. and Filpula, D.R.

Production of engineered igM-binding single-chain antibodies in
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larity 78.6%;
Conservative
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                /gene="7A4-1/212"
<1. .735
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antibody Bet 2 (ATCC HB88)"
313...354
                                                      /db_xref="taxon:29278"
1. 735
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LIFNTNSLQTGIPSRFSGSGSGTDYTLTISGLQPEDVATYFCYQYKNGYTFGAGTKLE
LKGSTSGSGKGSEGKGEVQLVESGGGLVQPGSSLKVSCVASRFTFSSYVMHWFRQAPE
NGIEWLAYINTDSSSAHYAETVKGRFTISRDNAKNTVDMQLSSLRSEDTAMYFCARGG
/gene="7A4-1/212"
                                                                                                                      Location/Qualifiers
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/function="binds mouse IgM"
/product="fusion protein"
/db_xref="PID:g310726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="artificial sequence"
/db_xref="taxon:29278"
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.717
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Pred. No. 0; Misma
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5.35e-02;
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RESULT 10
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DEFINITION
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AUTHORS
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MEDLINE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 AGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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g310739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \ensuremath{\mathsf{IgM}}\textsc{-binding} protein; fusion protein; fusion monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95336669
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1 (bases 1 to 744)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Production of engineered IgM-binding single-chain antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagle, J.W. and Filpula, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee, T.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 57.1%;
Similarity 78.6%;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ind. Microbiol. 14 (5), 371-376 (1995)
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                                                                                                                                                                                                                            /transl_table=11
/function="binds human IgM"
/function="binds human IgM"
/product="fusion protein"
/db_xref="piD:g310740"
/db_xref="piD:g310740"
/translation="buvMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSNQKNYLAWYQQKTAMSPATIONSTATESGVPDFTIGSGSGTDFTLTISSVQAEDLADYFCQQHYSTPF
TFGSGTKLEIKGSTSGSGKSSEGKGQVQLQQPGAEFVKPGAPVKLSCKASGYPFTTYW
VNMMKQRPGRGLEWIGRIDPTDSETLYNQKFKDKATLTVDKSSSTAYIQLSSLTSEDS
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a 176 c
/note=1
                                                                    340.
                                                                                                 /note="variable light chain antibody DA4.4 (ATCC HB57)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="7A4-1/212"
/note="synthetic linker"
382. .735
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/transl=17A4-1/212 SCA fusion protein"
/product="7A4-1/212 SCA fusion protein"
/db_xref="PID:9207840"
/translation="DVVMTOTPSSLAMSVGQKVTMSCKSSGSLLNISNQKNYLAWYQQ
KPGQGSPKLLYFASTRESGYDERFIGSGSGTDFTLTISSVQAEDQADYFCQQHYRAPR
TFGGGTKLEIKGSTSGSGKSSEGKGQVQLVESGPGLVAPSQSLSITCTVSGISLSRYN
VHWVPQSPGKKLEWLGMIWGGGSIEY.NPALKSRLSISKDNSKSQIFLKMNSLQTDDSA
                                                                                                                                                                                                      AVYYCARETYDYPFAYWGQGTLVTVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="artificial sequence"
/db_xref="taxon:29278"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /standard_name="DA4.4/212 sFv protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="7A4-1/212"
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                                "linker segment"
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1. No. 5.35e-02;
Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hallberg, P.L., Oelkuct, M.S.,
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                                                                                                                                           7 GATTTACCAGAAGCAGAGGAAGAA 30
                                                                                                                                 GATTTACCAGAACCAGAGGTAGAA 325
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Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liliopsida; Poales; Poaceae; Hordeum.

1 (bases 1 to 228)
Martin,M., Casano,L.M. and Sabater,B.
Identification of the product of ndhA gene as a thylakoid protein synthesized in response to photooxidative treatment plant Cell Physiol. 37 (3), 293-298 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chloroplast,
S82816
Chloroplast Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry [NCBI gibbsq 179114] from This sequence comes from Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S82816 228 bp DNA ndha=NDH-A [Hordeum vulgare=barley,
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33; Conser
                        NDH-A protein; ndhA gene.
                                        g2239133
                                                    Y13729
                                                               Hordeum vulgare
                                                                             HVNDHA590
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              Hordeum vulgare.
                                                                                                                                                                                   Similarity
22; Conser
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larity 78.6%;
Conservative
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a 187 c
                                                                                                                                                                                                                                               /db_xref="PID:g1754725"
/translation="PFDLPEAGELVAGYQTEYSGIKYGLFYLVSYLNLLVSSLFVTV
LYLGGWNFSIPYISFFDFQMKAVGILEMTM"
15 c 38 g 92 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="variable heavy chain derived from mouse monoclonal
antibody DA4.4 (ATCC HB57)"
187 c 186 g 179 t
                                                                                                                                                                                                                                                                                                                                                                              'note="NDH-A"
'gene="ndhA"
                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                 'product="NDH-A"
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91.7%;
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ce chloroplast
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1. No. 5.35e-02;
                                                                                                                                                                                Mismatches
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ig. 1.
                                                               DNA for ndhA gene 3'end (exons 1 & 2).
                                                                                                                                                                                               8.14e+00;
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                                                                                                                                                                                   2;
                                                                                                                                                                                                          Length 228
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Query Match
Best Local Similarity
Chas 22; Conserv
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                                                                                                                                      Hordeum vulgare. Chloroplast Hordeum vulgare Chloroplast Hordeum vulgare Eukaryota; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Embryophyta; Lillopsida; Poales; Poaceae; Hordeum Magnollophyta; Lillopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-JUN-1997) Sabater B., Biologia Vegetal, Fac. Ciencias, Campus Universitario, Universidad de Alcala de Henar Cra. Madrid-Barcelona km 33,6, Alcala de Henares. Madrid 28871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcript editing in several gram Plant Physiol. 115, 313-313 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sabater, B.
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Embryophyta; vascular plants; seed plants; Magnoliophyta
Liliopsida; Poales; Poaceae; Hordeum.
1 (bases 1 to 590)
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Hordeum vulgare chloroplast
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ilarity 91.7%;
Conservative
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/translation="SNSSSTVDIVEAQSKYGFFGWNIWRQPIGFLVFLISSLAECERL
PEDLPBAEEELVAGYQTEYSGIKYGLFYLVSYLNLLVSSLFVTVLYLGGWNFSIPYIS
FFDFFQMNKAVGILEMTMGIFITLTKAYLFLFISITIRWTLPRMRMDQLLNLGWKFLL
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                                                                       Kremsdorf,D., Favre,M., Jablonska,S., Obalek,S., Rueda,L.A., Lutzner,M.A., Blanchet-Bardon,C., Van Voorst Vader,P.C. and Orth,G. Molecular cloning and characterization of the genomes of nine newly recognized human papillomavirus types associated with epidermodysplasia verruciformis J. Virol. 52 (3), 1013-1018 (1984)
                                                                                                                                                                                                                                                                                                                               Human papillomavirus type
Human papillomavirus type
Viruses; dsDNA viruses, no
Papillomavirus.
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A comparative
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                                    (bases 1 to 7368)
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tive analysis of group II introns
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Pred. No. 8.14e+00;
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HPV22 was originally isolated from macules on the chest of an Italian epidermodysplasia verruciformis (EV) patient [2]. The HPV22 genome, like that of HPV9 9, 15, 17a/b, 23, 37, 38, is smaller than most PV genomes at approximately 7.4 kb. Phylogenetic reconstructions based on DNA sequences of established types indicate that HPV22 is most closely related to HPVs 23 and 38, and then to 15, 17, 37 and 9. Although Kremsdorf et al [2] found substantial cross-hybridization between HPV22 and HPV19, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence comparison fails to support a close relationship between
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                                                                                                                                                                                                                                                                                                     ESDVSDLINDDTAAQGNSRELLCQQQSEECEQQIQYLKRKYFSPKAVQQLSPRLQSM
NISPGHKSKRRLFVEHDSGLECSLNBAEDLTEEVEVBAAPAPAAQGCYGSGHYTSLL
RCNNVKAVLLGKFKDAFGVSYNGLTROFESNKTCCKHWVLAIYAAKDBLIDASKQLLQ
QHCTYLMLQTFSPMSLYLCCFNVGKSRETVMRLLSSMLQVNENHILSEPPKIRSMIAA
LFWYKGSMNPNVAFGEYPEMINTQTMIHQTASVQFDLSEMIQWAYDQDYVDECTI
AYQYAKLADSMSNARAFLAHNSQAKYVRECAQWYRYYKREENBOMSISAWIHHGISK
EGDGHWQDIVKFLRYQGLNFIVFLDKFRTFLKNFPKKNCLLICGPPDTGKSMFSMSIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="E1"
932. .2758
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KSPPADCFKKGPKSVEVYFDGDPENVMSYTVWSYIYYQTDDESWEKVEGHVDYTGAYY
                                                                                                                                                                                                                                           KALRGOVVSFANSKSHFWLQPLADAKLALLDDATEVCWQYIDAFLRNGLDGNMVSLDM
KHRAPCQMKFPPLIITSNISLKKEKKFPYLHSRIYEFEFPNKFPFDANDTPLFKLTDQ
SWASFFKRLWTQLELSDQEEEGENGETQRTFQCTTREVNGLI"
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/taanslation="%1560ATLCDIVLEELVLPIDLHCHEELPELPEELEESVVEEEP
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EYTPYKIVYCGGCDTKLKLYILATLSGIRDFQTSLLGPVKLLCPTCREEIRNGRR"
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643. .945
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="replication protein E1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKAIE"
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                                                                                                                                      'note="putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:37954"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Human papillomavirus type 22"
note="cloned HPV-22 was obtained from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="E7"
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RESULT
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Best Local S
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                                                                    Chlamydia trachomatis. Chlamydia trachomatis
   Eubacteria; Chlamydia
1 (bases 1 to 13316)
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/gene="L2"
4077
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CIPCLGSYWDKAPVCEDAGSQVGLCPPLELKNGVIEDGDMFDIGGNINNKTLSFNRS
CIPCLGSYWDKAPVCEDAGSQVGLCPPLELKNGVIEDGDMFDIGGNINNKTLSFNRS
DVSLDIVNEIGKYPDFTMSNDVYGDSCFFCARREQCYAFNIFVRGGLVGGLNGDAIPDSAG
DVSLDIVNEIGKYPDFTMSNDVYGDSCFFCARREQCYAFNIFVRAGGLWGDAIPDSAG
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QDHKYYLPAAGGTALHNG
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YGSVGVFFGGLGISTGKGTGGFTGYIFLGGGGGGVGVKGATPTVVFGGVIFEIIGFTELI
PVDSVTPIDPAAPSIVTLTDSSAGADLLPGEVETIAFVHPFDUVELDFFLVGGDFH
AILEVTDANPPFRRTVTRTQYHNPAFEIISESTPLIGESTPSDHVFVFEGSGGVQVGD
ANESIELDTFPSRYSFDIEEPFPPRKYSTPIERISQEFRTLREALYNRRLTEQYQVRD
PLFIRSPSRLVJRFOFEDNFUDEETJOIFERDVAAVEEPPRODFLDIERLGRFPILTET
PLFIRSPSRLVJRFOFEDNFUDEETJOIFERDVAJVEEPPRODFLDIERLGRFPILTET
EGRYRVSRLGQRASLSTRSGARVGARVHFFTDISTINAEEPIELELLGEHSGDSSVYQ
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GRATRRSLSRESAESPRRGGRGGGFLTRSRSRSRSRTRESVDGGGVAPDEVGATLRS
IGRQHSGRLAQLLDAAKDPPVILLRGAANTLKCYRYRFRKKHAGSFQFISTTWSWVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLTQI NAMNHG I LENWQLGFVPTPDNSVHDTYRYLQSKATKCPDAVPDTQKEDPFGQY
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PSITVPQFESPRETIVYIQDIEGNTVVYPKYEERPTIILPTPSGPAIIQSPTHSSFDY
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KPDQGPEAPSSGEGGPPDDPSPENPQNPPGGEGEVEGAPSPGPAQGRDPVHESLLTGV
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/db_xref="PID:g1020184"
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/gene="L2"
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                                   Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                13316 bp
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Pred. No. 8.14e+00;
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33 of 87 of the complete genome.
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AUTHORS
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2 (bases 1 to 13316)
Stephens, R.S., Kalman, S., Lammel, C.J.,
Aravind, L., Mitchell, W.P., Olinger, L.,
Koonin, E.V. and Davis, R.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-MAY-1998) Program of California, 235 Warren Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stephens,R.S., Kalman,S., Lammel,C.J., Fan,J., Marathe,R., Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koonin, E.V. and Davis, R.W. Genome Sequence of an Obligate Intracellular Pathogen of Humans:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fan, J., Marathe, R., Tatusov, R.L., Zhao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, Q.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGHSVIIIEHNMHVVKVADYILELGPEGGNKGGYLIASCSPEELIHKHTPTAIALRPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Excinuclease ABC Subunit
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gene

CDS

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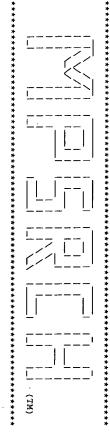
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BASE COUNT
ORIGIN
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Best Local S
Matches 2
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331 CTCTGGTTCTGGTAAATCTTCT
                                                                                     h 47.6%;
Similarity 95.5%;
21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLPQEEVEHEISRYYKALKRSRSDLAALEKEAKGKQGYQEIASILQAHLEIIKDPLLT
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Pred. No. 8.14e+00;
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Search completed: Sat Jan Job time: 107 secs. φ 17:12:39 1999 Ş

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Sat Jan 9 17:20:30 1999; MasPar time 20.09 Seconds 284.402 Million cell upda updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: (322-363) from US08704178.seq (4 of 4) 42 >US-08-704-178-1

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Scoring table: TABLE default Gap 6

Gap

Nmatch Searched: STD: 188442 seqs, 68026449 bases Dbase 0; Query 0

× 2

Post-processing: Minimum Match 0% Listing first 45 summaries

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
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24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
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Statistics: Mean 5.992; Variance 4.139; scale 1.448

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ding the Fv cDNA.  anti-erb ding a 4 chain an chain an anti-erb ding the dding a m	66.7 744 7 Q43288	90.5 720 9 Q55181 90.5 731 7 Q43287 90.5 770 7 Q43290 76.2 91 9 Q51746	Q55180 T17728 T65006 Q43289 Q14831 T65007	Result Query No. Score Match Length DB ID Description
	Sequence encoding a m Oligonucleotide probe	encoding encoding encoding leotide pr	15 10 1	Description

Query Match 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative

Score 42; DB 9; L Pred. No. 4.08e-12; 0; Mismatches 0

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Q04525 N90964 Q06496 Q06831	OJ 4P	Q50946 Q51556	T99264 T99140	Q46603 Q44800	N70608	T97296	Q21678	Q38251	Q62663	Q22963	Q66840 043292	080512	Q11195	049187	T86394	Q55841	Q43293	Q43291	CODET.
Total base sequence o Sequence in a recombi IFN-alpha 61 gene and Sequence encoding B.t	steroid rece en leucocytoz	Sequence encoding pro Sequence encoding pro	Human PUR-alpha gene. Full length cytochrom	Mixed oligonucleotide Encodes single-strand	Mouse additional sex VISNA sheep lentiviru	se additional sex	- recor	HCV CKS-33-BCD fusion	3 2	of pHCV-31	4-4-20 VL/ 217 / CC49	Primer used in immuno	Ballast Constituent c	scFvR construction pr	Sp6 anti-TNP antibody	-21//4-4-	Si	encoding	/212 SCA
9.18e+00 2.57e+01 2.57e+01 2.57e+01	.18	.18	9.1	9.18	ω ω	. 21	1:		1.10e+00		1.10e+00						.00e-	.29e-	. 29e-0

## ALIGNMENTS

SQ	38	8	38	റ്റ	გ	റ്റ	PS	ΡŦ	ΡŢ	ΤĠ	DR	DR	ΡI	PA	PR	ΡF	g	ΡN	ŦΤ	ŦΤ	H3	S	ΚW	ΚW	DE	DŢ	AC	Ħ	RESULT
Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;	animals given a combination of the 2 Abs, tumours completely	growing tumours were used in a trial of the efficacy of the Abs. In	erbB-2). Abs no. 21 and 23 are directed against the extracellular	engineered to express the human erbB-2 protein on its surface (N/	23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell	The source of human erbB-2 protein for the prodn. of antibodies no.	Example; Fig 7; 37pp; English.	gp185	2 monoclonal antibodies which recognise different epitopes on	Treatment of malignancies over-expressing ERB-[2 - using at least	P-PSDB; R45442.	WPI; 94-025878/03.	Kasprzyk PG, King CR;	(MOLE-) MOLECULAR ONCOLOGY INC.	30-JUN-1992; US-906555.	21-OCT-1992; U08545.	06-JAN-1994.	WO9400136-A.	/*tag= a		Key Location/Qualifiers	Synthetic.	monoclonal antibody; ss.	Single chain anti-erbB1 antibody; cancer therapy; prevention;	Sequence encoding the single chain anti-erbB2 antibody, Ab no.23.	21-JUL-1994 (first entry)	Q55180;	Q55180 standard; cDNA; 711 BP.	LT 1

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Matches
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24-DEC-1996.
07-OCT-1991: 772270.
07-OCT-1991: US-772270.
30-JUN-1992: US-906555.
14-MAY-1993: US-061092.
              Bird RE,
WPI; 97-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 42; Page 29-30; 48pp; English.

A nucleic acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a single chain Fv fragment (R94020) that binds a human erbB2 oncoprotein. The anti-erbB2 SFv portion is obtained by PCR using e33scFv plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibody homologue within e.g. an epithelial carcinoma cell. Intracellular expression of the homologue inhibits surface expression of erbB2 and thereby inhibits cell proliferation and cell survival and decreases
                                                                                                                                                                                                                                  05-JUN-1997 (first entry)
Single-chain anti-erbB2 antibody e23(Fv) cDNA.
Single chain antibody: variable region; light chain; heavy
breast cancer; ovarian cancer; non-small cell lung carcinom
                                                                                                                                                                                                                                                                                   T65006 standard: cDNA;
T65006;
05-JUN-1997 (first ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uncoprotein; erbB2; cell proliferation; tumour; cancer;
intracellular antibody homologue; single chain antibody; scFv;
gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibition of proliferation or survival of, esp. malignant erbB2, cells - by introducing nucleic acid mol. encoding antibody homologue which is expressed and binds, pref. erbB2, protein intracellularly
                                                                                                                                                                                                                 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumorigenicity.
Sequence 711 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Curiel DT, Deshane J; WPI; 96-171307/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-1996.
23-AUG-1995; U10740.
06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
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Anti-erbB2 scFv cDNA.
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                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                               immunodiagnosis;
                                        (ARON-) ARONEX PHARM
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Curiel DT, Deshane J;
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Local Similarity 100.0%;
nes 42; Conservative
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RE, Kasprzyk PG,
97-064831/06.
DB; W15185.
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/*tag=
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1..711
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                          King CR;
                                                                                                                                           e23(Fv)
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Pred. No. 4.(
0; Mismatch
                                                                                                                                                                                                                           er; non-small cell lung carcinoma; cytotoxic agent; erbB-2; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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4.08e-12;
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Example 8; Columns 25-28; 28pp; English.

The present cDNA sequence codes for a claimed single-chain antibody, designated e23(FV), which binds to erbB-2. Monoclonal antibody e23 was generated by immunising mice with N/erbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light-chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gpl85 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours.

Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                     New multivalent antigen-binding protein e.g. contg. CC49) regions - useful in diagnosis, for destroying blood clots targetting cytotoxic agents or enzymes to tumour cells Example; Fig 15A; 118pp; English.

Free cysteines were engineered into the C-terminal of the 4-4-20/212 single-chain antigen-binding protein, in order chemically crosslink the protein. The design was based on hinge region found in antibodies between the CH1 and CH2 in the control of t
                             In order to try to reduce antigenicity in humans, the him sequence of the most common 1gG class, 1gGl, was chosen design for the hinge region, the C-terminal serine in the 4-4-20/212 singl-chain antigen-binding protein was made the serious control of the himself of the serious control of the serio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood JF;
WPI; 93-196999/24.
P-PSDB; R37647.
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20-NOV-1992; U09965.
25-NOV-1991; US-796936.
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Sequence encoding a 4-4-20/212 single-chain antigen-binding
protein with a single cysteine hinge.
Antibody; multivalent; variable region; heavy chain; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cds
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27-SEP-1993
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Q43289 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ENZO-) ENZON INC.
Bird RE, Filpula
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Similarity 100.0%;
42; Conservative
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gen-binding protein was made the first second residue of the hinge was changed
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Pred. No. 4.08e-12;
0; Mismatches 0;
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g blood clots and
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based on the
and CH2 regions
                                                                                                   the hinge chosen. In t
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14-NOV-1991; U03149.
07-MAY-1991; U03149.
08-MAY-1990; US-521258.
18-JUN-1990; US-539980.
                                                                               05-JUN-1997
Single-chain
Single chain
                                                                                                                                                                                                                                                                                                                                              Disclosure: Fig 1; 73pp; English.

The sequence encodes Qm212, a single chain antigen binding protein having a metal binding site which is derived from the 4-4-20/212 protein (Bird et al., Science, 242:423-426 [1988]), Qm212 differs from 4-4-20/212 by amino acid substitutions at residue positions 60, 62, 115 and 117 to provide for contact amino acid residues, where three of these contact residues form a metal binding site. The organism form which the gene originated is not given in the specification. The protein may be used to selectively partition and/or remove metal-protein complexes from a liquid phase or as be used to remove metal-protein complexes from a liquid phase or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q14831;
17-FEB-1992 (first entry)
0m212 single chain antigen binding protein with metal binding site.
Antigen binding; metal cations; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from a cysteine to a serine. The hinge regions were added by introduction of a BstE II restriction site in the 3^{\prime}-terminus of the gene encoding the 4-4-20/212 single-chain antigen-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCRI-) SCRIPPS CLINIC & RE.
Lerner RA, Roberts VN, Getzoff ED,
WPI; 91-353518/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q14831
mat_peptide
                            Synthetic.
                                          Mus
                                                                  breast cancer;
                                                                                                                       T65007
                                                                                                                                                                                                                                                                                                  indicators of metal complex formation. The metal-protein complexes can also be used to promote a predetermined chemical reaction, e.g. hydrolysis of a peptide bond.

Sequence 803 BP; 224 A; 175 C; 197 G; 207 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New metal binding proteins - immunoglobulin and 3 contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; R15055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                       immunodiagnosis;
                                                                                                                                   T65007 standard;
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                                                                                                                                                                                          322
                                          musculus.
                                                                                                                                                                                          AGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG
                                                                                                                                                                                                       aggttctacctctggttctggtaaatcttctgaaggtaaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                    100.0%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
Similarity 100.0%;
                                                           anti-erbB2 antibody e21(Fv) cDNA.
antibody; variable region; light chain; heavy charithous; non-small cell lung carcinoma; ovarian cancer; non-small cell lung carcinoma;
                                                                                                         (first entry)
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
 Location/Qualifiers
1..720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                     treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ø
                                                                                                                                                                                                                                                         Score 42; DB 3; Pred. No. 4.08e-12
                                                     cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 7; 1
Pred. No. 4.08e-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising aminoacid r
                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tainer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7;
                                                     agent; erbB-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ც</u>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Benkovic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 761;
                                                                                                                                                                                                                                                                      Length 803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                              0
                                                                                                                                                                                          363
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as metal
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al binding
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                                                                                 chain;
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Strample 9; Columns 27-39; 28pp; English.

Chairment odn sequence codes for a calaimed single-chain antibody e21

Cdesignated e21(Fv), which binds to erbB-2. Monoclonal antibody e21

Cwas generated by immunising mice with N/erbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gpl85 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours.

Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-DEC-1996.
07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q55181 :
Q55181;
                             The source of human erbB-2 protein for the prodn. of antibodies no. 23 and 21 (055180/R45442; 055181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. In animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
                                                                                                                                                                                                                                                                06-JAN-LJY:
21-OCT-1992; U08545.
30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ARON-) ARONEX PHARM INC. Bird RE, Kasprzyk PG, King WPI; 97-054831/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1994 (first entry)
Sequence encoding the single chain anti-erbB2 antibody, Ab no Single chain anti-erbB1 antibody; cancer therapy; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Columns 27-30; 28pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single chain antibodies specific labels or cytotoxin, useful for c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W15186
                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody; ss.
                                                                                                                                                                                                      Treatment of malignancies over-expressing ERB-[2 - using at least 2 monoclonal antibodies which recognise different epitopes on
                                                                                                                                                                       Example; Fig 8; 37pp;
                                                                                                                                                                                                                                      P-PSDB; R45443
                                                                                                                                                                                                                                                      Kasprzyk PG, King
WPI; 94-025878/03.
                                                                                                                                                                                                                                                                                                                                                     WO9400136-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 aggttctacctccggatctggtaaatcttctgaaggtaaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..171
                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= e21(Fv)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.5%;
95.2%;
   90.5%;
                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              720
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 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 29;
Pred. No. 6.29e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain anti-erbB2 antibody, Ab no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erbB-2
   B
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and treatme
 9
Length 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 720
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Best Local S
Matches 4
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-1993.
20-NOV-1992; U09965.
25-NOV-1991; US-796936.
(ENZO-) ENZON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         targetting cytotoxic agents or enzymes to tumour cells

Example: Fig 10A; 118pp; English.

"4-4-20 VL" means the variable region of the light chain of the
4-4-20 mouse monoclonal antibody (Bird, R.E. et al., Science 242:423
(1988)). The number "212" refers to a specific 14-residue
polypeptide linker that links the 4-4-20 VL and the CC49 VH. See
Bedzyk, W.D. et al., J. Biol. Chem. 265:1865-18620 (1990). "CC49 VH"
is the variable region of the heavy chain of the CC49 antibody,
which binds to the TAG-72 antigen.
Sequence 731 BP; 190 A; 176 C; 180 G; 185 T;
                                                                                          Antibody;
linker; se
                                                                                                          Sequence encoding a 4-4-20/212 single-chain antigen-binding protein with the two cysteine hinge. Antibody; multivalent; variable region; heavy chain; light
                                                                                                                                                                                Q43290 standard; DNA; 770
Q43290;
27-SEP-1993 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding a multivalent antigen-binding comprising the 4-4-20 VL region connected through polypeptide to the CC49 VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cds
                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q43287;
27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q43287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New multivalent antigen-binding regions useful in diagnosis, f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; R37645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; multivalent; linker; ss.
                                                                                                                                                                                                                                                                                                                                                              336
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                                                                                                                                                                                                                                                                                                                       322
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                          SS
                                                                                                                                                                                                                                                                                                                                                                                                          40;
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                                                                                                                                                                                                                                                                                                                                                                                                      90.5%;
llarity 95.2%;
Conservative
                                                                                                                                                                                (first entry)
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379..723
/*tag=
Location/Qualifiers
1..765
/*tag= a
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337..378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hardman K,
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                                                                                                                                                                                                                              ВΡ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 linker
                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 7; I
Pred. No. 6.29e-10;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for destroying blood clots and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               connected through the 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĭ
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Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rollence M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy
                                                                                                             chain; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                        2,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 731;
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                                                                                                                                                                                                                                                                                                                                                            377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single-chain protein
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                             Synthetic.
EP-571911-A.
01-DEC-1993.
24-MAY-1993;
26-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              In order to try to reduce antigenicity in humans, the hinge sequence of the most common IgG class, IgG1, was chosen. In the design for the hinge region, the C-terminal serine in the 4-4-20/212 singl-chain antigen-binding protein was made the first serine of the hinge and the second residue of the hinge was change from a cysteine to a serine. The hinge regions were added by introduction of a BstE II restriction site in the 3'-terminus of the gene encoding the 4-4-20/212 single-chain antigen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New multivalent antigen-binding protein e.g. contg. CC49 Mab regions - useful in diagnosis, for destroying blood clots and targetting cytotoxic agents or enzymes to tumour cells Example; Fig 15B; 118pp; English.

Erree cysteines were engineered into the C-terminal of the Free cysteines were engineered into the C-terminal of the 4-4-20/212 single-chain antigen-binding protein, in order to chemically crosslink the protein. The design was based on the hinge region found in antibodies between the CH1 and CH2 regions.
                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide probe MK14-A Oligonucleotide; DNA probe; m
              Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.
                                                                                                                                                                                                           (BECT ) BECTON DICKINSON CO
Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                            New oligo:nucleotide probes detection and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cds
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Claim 3; Page 14; 23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1994
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20-NOV-1992; U09965.
25-NOV-1991; US-796936.
(ENZO-) ENZON INC.
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larity 95.2%;
Conservative
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379..729
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                                                                                                                                                            specific for Mycobacteria of Mycobacteria nucleic a
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Pred.
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6.29e-10;
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Example; Fig 108; 118pp; English.

C 44-20 VH" means the variable region of the heavy chain of the current consistence of the second consistence of the second consistence of the current current consistence of the current consistence of the current current consistence of the current current current current consistence current c
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Q51746;
31-MAY-1994
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Q43288;
Q43288;
27-SEP-1993
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Antibody; multivalent; variable region; heavy ch linker; ss.
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Synthetic.
EP-571911-A
                                                     Oligonucleotide;
                                                                      Oligonucleotide probe MK14-A
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10-JUN-1993.
20-NOV-1992; U09965.
25-NOV-1991; US-796936.
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Bird RE, Filpula D,
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                                                                                                                              standard;
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larity 83.3%;
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340..381
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                                                     DNA probe; mycobacteria;
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Pred. No.
35; Misma
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Pred. No. 1.24e-04;
0; Mismatches 7
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No. 1.03e-06
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the 212 linker
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Best Local Similarity
Matches 0; Conser
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Best Local
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25-APR-1996;
13-OCT-1995; U12840.
13-OCT-1994; US-323445.
(ENZO-) ENZON INC.
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24-MAY-1993;
26-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           729058;
03-0CT-1996 (first entry)
CC49/212 SCA PLAP DNA construct.
Single-chain antigen-binding fusion protein;
cytostatic; phospholipase A activating protei
therapy; monoclonal antibody; CC49; ds.
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5.A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                              New antigen binding proteins contg. immunoeffector or cytolytic peptide - attached to variable regions of antibody light or heavy chain, useful in diagnosis and in destroying cancer cells Example 1; Fig 4A-B; 72pp; English.

A novel DNA construct (T29058) codes for a single-chain antigen-binding fusion protein (R97380) comprising the light chain variably region (VL) of monoclonal antibody CC49 linked to the CC49 VH region via a spacer peptide (R97379). With a C-terminal phospholipase A activating protein (FDAP) immunoeffector peptide (R97368). It was obtd. by ligating a synthetic PLAP fragment to a existing CC49/212 gene, and can be used to produce the fusion protein in transformed host cells. The fusion protein combines
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Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                 protein in transformed most certain the tumour antigen-binding capability of CC49 with immunoeffector function of PLAP.

203 C: 195 G;
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                                                                                               Similarity 78.6%, 33; Conservative
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78.6%;
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No. 4.10e-03;
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1.29e-02;
2.29;
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25-APR-1996: U12840.
13-OCT-1995: U12840.
13-OCT-1994: US-323445.
(ENZO-) ENZON INC.
Filpula D. Shorr R. Whitlow M;
WPI: 96-221949/22.
P-PSDB: R97381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antigen binding proteins contg. immunoeffector or cytolytic peptide - attached to variable regions of antibody light or heavy chain, useful in diagnosis and in destroying cancer cells Disclosure; Page 39-40; 72pp; English.

A novel DNA construct (T29059) codes for a single-chain antigen binding fusion protein (R97381) comprising the light chain variable region (VL) of monoclonal antibody CC49 linked to the CC49 VH region via a spacer peptide (R97379) and with an N-terminal phospholipase A activating protein (PLAP) immunoeffector peptide (R97368). It can be used to produce the fusion protein in transformed host cells. The fusion protein combines the tumour antigen-binding capability of CC49 with the immunoeffector function of PLAP.
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PIAP CC49/212 SCA DNA construct.
Single chain antigen-binding fusion protein; SCA; immunoeffector; cytostatic; phospholipase A activating protein; PLAP; cancer; therapy; monoclonal antibody; CC49; ds.
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Similarity 78.6%;
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427..1065
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10 10-JUN-1993.

11 20-NOV-1991; US-796936.

12 ENZO. NEZON INC.

13 Mood JF; Sipula D, Hardman K, Rollence M, Whitlow MD, Wood JF; Wood JF;
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Search completed: Sat Jan Job time: 25 secs. 9 17:20:55

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	sequ 6.51e pred 6.51e 1.05e	to have a being printed tion.		91:0		,		ω	algorithm Seconds ll updates	h Unit. U.K.	[M]

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# ALIGNMENTS

Query Match Best Local Matches	FEATURES SOURCE BASE COUNT ORIGIN	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM
47.6%; Score 20; Similarity 85.2%; Pred. No. 23; Conservative 0; Misma	Location/Qualifiers 1. 243 2019anism="Fugu rubripe/db_xref="taxon:31033" /clone_1ib="cosmid 1846 /clone="184617aD8" clone="184617aD8" 33 g		Teleostei; Eutracoo; Chordata Teleostei; Eutracoo; rmes; Tetracoo; o 243) rk,M., Smith,S nd Brenner,S. sion -JUN-1998)·MRC	FR0033790 243 bp DNA Fugu rubripes GSS sequence, clone sequence. AL030157 g3272271 g3272271 gSS; genome survey sequence. Fugu rubripes Fugu rubripes
DB 27; Length 243; 6.51e-05; atches 4; Indels 0; Gaps 0;	s" 17" 93 t 8 others	SB, UK. Email:	a; Vertebrata; Actinopterygii; percomorpha; eleostel; Acanthopterygii; percomorpha; ntoidei; Tetraodontidae; Fugu, Meek,S., Warner,S., Umrania,Y., Human Genome Mapping Project Resource	243 bp DNA GSS sequence, clone 184G17aD8, genomic survey irvey sequence.

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SOURCE
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Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 477)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S
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Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Schee, M.C. and Eun, M.Y.
Large-scale Sequencing Analysis of ESTs from Unpublished (1998)
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97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
cDNA clone 97SN1787, mRNA sequence.
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/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: Eco:
XhoI; Directional cDNA library inserted into
xhoI; S'end with EcoRI and 3' end with X'
vector at 5'end with EcoRI and 3' end with X'
/db_xref="taxon:4530"
/clone="97SN1787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
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                                                                                                                                                                                                                   Soares pregnant uterus NbHPU
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6.51e-05;
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Homo sapiens cDNA clor
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                Geisel, G., Jost, S.
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into lambda ZAPII
ith Xho I site."
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                                         yn91f01.r1
A45036 PUR
                                  midbrain, pons and
                                                                                                                                                                                                                                                             55-year old male. 1st oligo(dT) primer [5'
                                                                                                                                                                                                                                                                            Homo sapiens clone=175801 library=Soares adult brain N2b5HB55Y vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI 55-year old male. 1st strand cDNA was primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -40ml3 fwd. ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway,
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llarity 88.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I
Site_2: Ecc RI; 1st strand cDNA was primed with a Not
oligo(dT) primer [5'
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88 c 96 ;
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/clone="506689"
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                                                                                                                                                                                                                                                                                                                                                                                                     217 bp mRNA EST 31-JUL-1995 Homo sapiens cDNA clone 175801 5' similar to SP:A45036 ALPHA=SINGLE-STRANDED-DNA-BINDING PROTEIN - ;.
                                    medulla
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Pred. No. 6.51e-05;
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                                                                                                                                                                                                                                                         1 (bases 1 to 229)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mc35f03.r1 Soares
5', mRNA sequence
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                                                                                                Contact: Marra M/Mouse EST Project
WashUrHHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                    Waterston, R.
The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
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Fax: 314 286 1810
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WashU-Merck EST Project
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                  Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse
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                                                                 Fax: 314 286 1810
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1. .217
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/clone="175801"
65 c 51 g 6
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80.0%;
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Pred. No. 1.05e-03;
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nes 27; Conse
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EST.
                                                                                                                         University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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AA754458
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: mob.REGA+ET
                                                                                                                                                                                                                   Suwon, Kyunggido, Ko
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                             Department of Cytogenetics National Inst. of Agri. Sci.
                                                                                                                                                                                                                                                                                                                            Large-scale Sequencing Analysis 
Unpublished (1998)
                                                                                                                                                                                                                                                                                               Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                           Poales;
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                                          /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Directional cDNA library inserted into lambda ZAPI vector at 5'end with EcoRI and 3' end with Xho I site."
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resist
             vector at 5'end with EcoRI and /db_xref="taxon:4530" /clone="97SN1784"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="350525"
                                                                                       /cultivar="Milyang23"
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                                                                                                         /organism="Oryza sativa"
clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.2%;
77.1%;
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C
                                                                                                                                                                                                                                                   Korea
                                                                                                                                                                                                                                                                                                                                                                          Yang, M.S.,
                                                                                                                                                                                                                                                                                                                                                                        Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 21;
Pred. No. 1.05e-03;
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                                                                                                                                                                                          Local
                                                                                               CTAACAATKGTYTTGGKWAGTTKGATGATGGTAAAGK 176
||| | | :||: |||::| | : ||| ||||||::
CTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG 363
                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01
       Mus
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D61368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho. Tokushima, Tokushima 771-01, Japan (Tel:0886-65-2888, Fax:0886-37-1035) submitted (30-May-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takada,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y. Unpublished(101)
                         C8,7905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
2 (bases 1 to 259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens cDNA to mRNA, clone_lib:Clontech human fetal brain polyA+ mRNA (#6535).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST: EST(expressed sequence tag); Human fetal brain; similar none(May 29,1995)
                                                                                                                                                                                                                                                                                                                                                                                                  Phone: 0886-65-2888
Fax : 0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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22; Conser
J05 337 bp mRNA musculus fertilized egg cDNA 3'-end
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fetal brain cDNA 5'-end GEN-184D07,
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                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Clontech'human fetal brain polyA+ mRNA
(#6535)"
35 c 45 g 80 t 26 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissuc_type="Immature Seed"
/dev_stage="5 days after pollination"
/dab_host="E. coli SOLE"
/lab_host="E. coli SOLE
16 c 21 g 34 t 169 ot
                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                        45.28;
                                                                                                                                                                      Score 19; DB 7;
Pred. No. 1.05e-03
6; Mismatches
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Pred. No. 1.05e-03;
22; Mismatches 9
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                                                                                                                                                                                                           Length 259
   sequence,
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   clone J0253E04
                     04-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 CCCTTACTTTAAAAATATTTCCCAGAACCACGGGT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                   High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seatt Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
AQ134058
g3525424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ134058 363 bp
HS_3056_A1_B09_MR CIT
sapiens genomic clone
                                                                                                                                                                                                                                                    1 (bases 1 to 363)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Shaker,R., Schmidt,S., Traicoff,R. and Hood,L.E. Construction of a Characterized Clone Resource for Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-JAN-1998) to the DDBJ/EMBL/GenBank databases. Hirofumi Doi, Doi Bioasymmetry Project, ERATO, Japan Science and Technology Corporation (JST); WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba-shi, Chiba 261-7112, Japan (E-mail:hddbioa.jst.go.jp, Tel:81-43-299-1351, Fax:81-43-297-7530) Location/Qualifiers
Sequence Tagged Connector Plate: 3056 row: C colu
                                                                                                                                                                      Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                  Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS.
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                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.2%;
Similarity 77.1%;
27; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Systematic analyses of genes expressed in fertilized mouse eggs(The ERATFO.Del Project at Wayne State University)
Unpublished (1998)
2 (bases 1 to 337)
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Mus musculus (strain:C57BL/6J) fertilized one-cell-emmanner.
EST(expressed sequence tag).
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DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mouse fertilized one-cell-embryo
/dev_stage="fertilized one-cell-embryo"
86 c 90 g 93 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="J0253E04"
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/strain="C57BL/6J"
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Pred. No. 1.05e-03;
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Plate=3056 Col-17 Row-C, genomic survey
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                                                                                                          Seattle,
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                                                                                                          WA 98109, USA
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                GTGCTACCTCTGGTCCTTCTAACTCTTCT 344
 GTTCTACCTCTGGTTCTGGTAAATCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
B46365
g2551199
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HS-1063-B2-B01-MF.abi
sapiens genomic clone
                                                                                                                                                                                                                                                                       Sequence Tagged Connector Plate: CT 796 row: D co. Class: BAC ends
High quality sequence sto
                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Zackrone University of Washington Seattle, WA 98195, USA Tel: (206) 616-8744 Fax: (206) 685-7301
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 411)

Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Mahairas,G.R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.

Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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                                                       45.2%;
larity 82.8%;
Conservative
                                                                                                                                                                                                                                                                         quality sequence stop: 411.
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larity 80.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                kzackron@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
47 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones
E-Coli DH10B"
                                                                                                                            /sex="M"
91 c
                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11;
E-Coli DH10B"
                                                                                                                                                       /db_xref="taxon:9606"
/clone="Plate=CT 796 Col=2 Row=D"
/clone_lib="CIT Human Genomic Spe
                                                                                                                                                                                                                            /organism="Homo sapiens"
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/clone="Plate=3056 Col=17 Row=C"
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Pred. No.
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Pred. No. 1.05e-03;
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CIT Human Genomic Sperm Library C Homo
Plate=CT 796 Col=2 Row=D, genomic survey
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Local Similarity 77.18;
nes 27; Conservation
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EST.
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                                                                                                                             AA104834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
WashUrMerck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ost Sarcopterygli; Choanata; Tetrapoda; Amniota; Mammalia; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Hd. (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
1 (bases 1 to 449)
Marra, M., Hillier, L.,
                             Snw
                                         Eukaryotae;
Vertebrata;
                                                                    house mouse.
Mus musculus
                                                                                                                                                         mp40f09.rl Barstead
                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stops:
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/clone="46914"
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                                        mitochondrial eukaryotes; Metazoa;
Eutheria; Rodentia; Sciurognathi; !
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Dietrich, N., Dubuque, T.,
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                                         ; Chordata;
Muridae; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                we'44030 473 bp mRNA EST 03-JUN-1997 ve'14h09.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone 832001 5' similar to gb:X58380 M.musculus HMGI-C mRNA for a nuclear phosphoprotein (MOUSE);, mRNA sequence.
                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Mur. Wertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Mur. Murinae; Mus. 1 (bases 1 to 473)

2 (bases 1 to 473)

3 (bases 1 to 473)

3 (bases 1 to 473)

4 (bases 1 to 473)

4 (bases 1 to 473)

4 (bases 1 to 473)

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High quality sequence stop: 414.
Location/Qualifiers
                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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WashIn-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                           The WashU-HHMI Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                house mouse
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Similarity 77.1%;
27; Conservative
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/dev_stage="6 weeks"
/lab_host="DH10B"
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/sex="mixed"
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134 c
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TITLE
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hes 26; Conservation
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         Gilbert Biology, Stanford, CA 94305
Tel: 650 723 3232
Fax: 650 725 8309
Email: fa.srl@forsythe.stanford.edu
                                                                                                                                                                      1 (bases 1 to 588)
Covitz,P.A., Smith,L.S. and Long,S.R.
Expressed sequence tags from a root h
truncatula cDNA library
                                                                                                            Contact: Long SR
Department of Biological Sciences and
                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                  Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Rutanae; Sapindales; Fabaceae; Papilionoideae;
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Medicago truncatula
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00521 MtRHE Medicago truncatula cDNA 5'
                                                                               Stanford University
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
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Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                          Medicago
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                                                                                              Institute
primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer: -28m13 rev2 ET from
h quality sequence stop: 335.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="832001"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares mouse
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156 c
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Pred. No. 1.05e-03;
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                                                               94305-5020,
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                                                                                                            Howard Hughes Medical
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RESULT 15
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JOURNAL
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Best Local Similarity 74.4%;
Matches 29; Conservative
                                                                                                                                   Query Match 45.2%;
Best Local Similarity 85.2%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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325 TTCTACCTCTGGTTCTGGTAAATCTTC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fugu rubripes.
Fugu rubripes
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
1 (bases 1 to 619)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One pass dye-terminator sequencing of cosmid cloned genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fugu rubripes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS; genome survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                   /organism="Fugu rubripes"
/ob_xref="taxon.31033"
/clone_lib="cosmid 184G17"
/clone="184G17bF10"
a 157 c 97 g 213 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
/cultivar="Jemalong"
/cultivar="Jemalong
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/dev_stage="2-3 day old seedlings"
110 c 135 g 168 t 3 others
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1. .588
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                                                                                                                               Score 19; DB 27;
Pred. No. 1.05e-03;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                 213 t
                                                                                                                                      4; Indels
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Search completed: Sat Jan 9 17:14:51 1999 Job time : 111 secs.

